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OM protein - protein search, using SW model

Run on: February 11, 2003, 18:21:26 : Search time 82 Seconds
(Without alignments)
30.875 Million cell updates/sec

Title: US-09-781-796b-7

Sequence: 1 KSDPTETGALDGGASQ 19

Scoring table: BLOSUM62
Gapop 10.0, Capext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
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11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	96	100.0	20	17	AAW04339
2	82	85.4	16	17	AAW04340
3	75	78.1	439	22	AAW70924
4	75	78.1	439	22	AAW70923
5	75	78.1	454	21	AAW70890
6	75	78.1	454	21	AAW70913
7	75	78.1	463	21	AAW70925
8	75	78.1	464	21	AAW70899
9	75	78.1	464	21	AAW70922
10	75	78.1	473	21	AAW70901

11	75	78.1	473	21	AAW70924	Human soluble CD39
12	75	78.1	474	21	AAW70900	Protein encoded by
13	75	78.1	474	21	AAW70923	Human soluble CD39
14	75	78.1	476	21	AAW70888	Protein encoded by
15	75	78.1	476	21	AAW70889	Human CD39-L4-1 pr
16	75	78.1	476	21	AAW70911	Human CD39-L4-2/3
17	75	78.1	476	21	AAW70912	Protein encoded by
18	75	78.1	478	21	AAW70891	Human soluble CD39
19	75	78.1	478	21	AAW70914	Protein encoded by
20	75	78.1	487	21	AAW70898	Human soluble CD39
21	75	78.1	487	21	AAW70921	Human CD39 protein
22	75	78.1	510	17	AAW04264	Human lymphoid cell
23	75	78.1	510	17	AAW04334	Human soluble CD39
24	75	78.1	510	21	AAW70887	Human soluble CD39
25	75	78.1	510	21	AAW70910	Human CD39
26	75	78.1	510	22	AAW71917	Human CD39-L66 pro
27	64	66.7	405	21	AAW44851	Human CD39-L4 prot
28	64	66.7	405	21	AAW72239	Human CD39-L4 vari
29	64	66.7	428	21	AAW44849	Human CD39-L4 vari
30	64	66.7	428	21	AAW44850	Human CD39-L4 vari
31	64	66.7	428	22	AAW72238	Human CD39-L4 vari
32	64	66.7	428	22	AAW72240	Human CD39-L4 vari
33	64	66.7	428	22	AAW72243	Human CD39-L4 vari
34	64	66.7	428	23	AAW19883	Human CD39-L4 vari
35	64	66.7	465	23	AAW19884	Human CD39-L4 vari
36	64	66.7	529	23	AAW19882	Human CD39-L4 vari
37	62	64.6	529	23	AAW76973	Human CD39-L4 vari
38	62	64.6	529	23	AAW53336	Human CD39-L4 vari
39	62	64.6	529	23	AAW53336	Human CD39-L4 vari
40	52	54.2	495	20	AAW33296	Human CD39-L4 vari
41	49	51.0	462	22	AAW30882	Human CD39-L4 vari
42	48	50.0	462	20	AAW55884	Human CD39-L4 vari
43	48	50.0	462	23	AAW78818	Human CD39-L4 vari
44	46	48.4	604	23	AAW18106	Human CD39-L4 vari
45	46	47.9	456	22	AAW93929	Human CD39-L4 vari

ALIGNMENTS

RESULT 1	AAW04339	standard; protein: 20 AA.
XX	AAW04339:	
AC	AAW04339:	
XX	29-DEC-1996 (first entry)	
DT	29-DEC-1996 (first entry)	
XX	ATP di-phosphohydrolyase fragment from pig pancreas.	
DE	ATP di-phosphohydrolyase: ATPase; bovine aorta; pig pancreas;	
KW	ATP di-phosphohydrolyase: ATPase; bovine aorta; pig pancreas;	
KW	ATPase; CD39; lymphoid cell activation antigen; enzyme;	
KW	platelet aggregation; thrombogenicity; anti-haemostatic.	
XX		
OS	Sus. scrofa.	
XX		
PN	W09632471-A2	
XX		
PD	17-OCT-1996.	
XX		
PF	10-APR-1996: 96WO-CA00223.	
XX		
PR	10-APR-1995: 95US-0419204.	
XX		
PA	(UYSH) UNIV SHERBROOKE.	
XX		
PI	Beaudoin AR, Sevigny J;	
XX		
DR	WPI: 1996-477122/47.	
XX		
PT	Isolated ATP di-phosphohydrolyase enzymes - have anti-haemostatic	
PT	activity, useful for reducing platelet aggregation and	
PT	thrombogenicity	

XX Claim 3: Page 46: 60pp: English.

XX The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
XX pancreatic (AAW04339) ATPases have been partially sequenced.
CC The sequences have been found to be highly homologous to a human
CC lymphoid cell activation antigen designated CD39 (Maliszewski et
CC al. (1994). J. Immunol.: 3574-3583). The complete sequences of the
CC ATPases types I and II have not been obtained yet. Assuming that
CC the CD39 gene product is an ATPase type II, the use of CD39
CC in the reduction of platelet aggregation and of thrombogenicity
CC may be contemplated, as well as a process of making ATPases
CC using the CD39 sequence (AA138516).

XX Sequence 20 AA:

Query Match 100.0%; Score 96; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSDTQETYGALDLGASTQ 19
DB 1 KSDTQETYGALDLGASTQ 19

RESULT 2

AAW04340
ID AAW04340 standard; Protein: 16 AA.

AAW04340:

29-DEC-1996 (first entry)

ATP diphosphohydrolase fragment (5) from bovine aorta.

ATP diphosphohydrolase; ATPase; bovine aorta; pig pancreas;
aprase; CD39; lymphoid cell activation antigen; enzyme;
platelet aggregation; thrombogenicity; anti-haemostatic.

Bos taurus.

MO9632471-A2.

17-OCT-1996.

10-APR-1996; 96MO-CA00223.

10-APR-1996; 95US-0419204.

(UTSH) UNIV SHERBROOKE.

Beaudoin AR, Sevigny J;

WPI: 1996-477122/47.

Isolated ATP di-phospho-hydrolase enzymes - have anti-haemostatic
activity, useful for reducing platelet aggregation and
thrombogenicity

Claim 2; Page 47: 60pp: English.

XX The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
XX pancreatic (AAW04339) ATPases have been partially sequenced.
CC The sequences have been found to be highly homologous to a human
CC lymphoid cell activation antigen designated CD39 (Maliszewski et
CC al. (1994). J. Immunol.: 3574-3583). The complete sequences of the
CC ATPases types I and II have not been obtained yet. Assuming that
CC the CD39 gene product is an ATPase type II, the use of CD39
CC in the reduction of platelet aggregation and of thrombogenicity
CC may be contemplated, as well as a process of making ATPases
CC using the CD39 sequence (AA138516).

XX Sequence 16 AA:

Query Match 85.4%; Score 82; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSDTQETYGALDLGGA 16
DB 1 KSDTQETYGALDLGGA 16

RESULT 3

AA71918
ID AAB71918 standard; Protein: 439 AA.

AA71918:

09-MAY-2001 (first entry)

Soluble human CD39 polypeptide.

Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;
stroke; thrombotic disorder; ischaemic disorder.

Homo sapiens.

MO200111949-A1.

22-FEB-2001.

11-AUG-2000; 2000MO-US22060.

13-AUG-1999; 99US-0374586.

(UYCO) UNIV COLUMBIA NEW YORK.

Pinsky DJ;

WPI: 2001-202805/20.

Treating stroke in a subject susceptible to intracranial hemorrhaging
and an ischemic disorder, involves administering a CD39 polypeptide
which inhibits ADP-mediated platelet aggregation or leukocyte
accumulation

Claim 3; Page 14: 118pp: English.

XX The present sequence is the active fragment of human CD39. CD39 or its
XX active fragment may be administered to treat or prevent stroke in a
XX subject susceptible to intracranial haemorrhaging or an ischaemic
XX disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
XX or leukocyte accumulation and/or ATP by increasing ADP catabolism to the
XX subject. CD39 or its active fragment is useful for treating or preventing
XX stroke, thrombotic disorders and ischaemic disorders such as peripheral
XX vascular disorder, pulmonary embolus, venous thrombosis, myocardial
XX infarction, transient ischaemic attack, unstable angina, reversible
XX ischaemic neurological deficit and sickle cell anaemia. It is also
XX useful for treating or preventing a stroke disorder in a subject
XX undergoing heart surgery, lung surgery, spinal surgery, brain surgery,
XX vascular surgery, abdominal surgery, or organ transplantation surgery.

XX Sequence 439 AA:

Query Match 78.1%; Score 75; DB 22; Length 439;
Best Local Similarity 73.7%; Pred. No. 0.00011;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETYGALDLGASTQ 19
DB 165 ETNNQETFGALDLGASTQ 183

RESULT 4
AA70890

ID AAV70890 standard; Protein: 454 AA.
 AC AAV70890;
 XX
 XX 17-AUG-2000 (first entry)
 DE Protein encoded by fusion construct of human soluble CD39 cDNA-1.
 KM Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KM unstable angina; myocardial infarction; stroke; coronary artery disease;
 KM atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KM platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KM cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KM cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KM peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KM PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KM occlusion; reocclusion; stenosis; restenosis; antilanginal; cardiatic;
 KM cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KM coronary ischaemia; vascular occlusion.
 KM Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX FT 1..15
 XX FT /label= Mature_human_interleukin_2
 XX FT /note= "N-terminal region"
 FT Protein 16..454
 FT /note= "human soluble CD39 protein"
 FT
 XX WO200023094-A2.
 XX 27-APR-2000.
 PD
 XX 13-OCT-1999; 99WO-US23641.
 PF
 XX 16-OCT-1998; 98US-0104585.
 PR 06-NOV-1998; 98US-0107466.
 PR 13-AUG-1999; 99US-0149010.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 DR WPI: 2000-339518/29.
 DR N-PSDB: AAD00201.
 XX
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides -
 PS
 XX Claim 6; Page 95-97; 118pp; English.
 XX
 XX The present sequence is the protein encoded by a fusion construct of
 CC sol(soluble)CD39 having apyrase activity. Fusion of 12 amino acids from
 CC the N-terminus of mature human IL2 to the solCD39 coding region results
 CC in high levels of both expression and activity in the supernatants of
 CC transfected cells. This is used in the treatment of unstable angina,
 CC myocardial infarction, stroke, coronary artery disease or injury,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
 CC platelet-associated ischaemic disorder including lung ischaemia, coronary
 CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
 CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke.
 CC
 XX Sequence 454 AA;

Query Match 78 18; Score 75; DB 21; Length 454;
 Best Local Similarity 73.78; Pred No. 0.00011;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OR 1 KSDPQENYGALDLGASTQ 19
 DB 180 EFNQETFGALDLGASTQ 198
 RESULT 5
 ID AAV70913 standard; Protein: 454 AA.
 AC AAV70913;
 XX
 XX 17-AUG-2000 (first entry)
 DE Human soluble CD39 and IL2 N-terminus comprising fusion construct.
 KM Soluble CD39; solCD39; human; apyrase activity; platelet activation;
 KM unstable angina; myocardial infarction; stroke; coronary artery disease;
 KM atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KM platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KM coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KM thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KM antilanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KM cardiatic; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
 KM Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX FT 1..15
 XX FT /label= Mature_human_interleukin_2
 XX FT /note= "N-terminal region"
 FT Protein 16..454
 FT /note= "human soluble CD39 protein"
 FT
 XX WO200023459-A1.
 XX 27-APR-2000.
 PD
 XX 13-OCT-1999; 99WO-US22955.
 PF
 XX 16-OCT-1998; 98US-0104585.
 PR 06-NOV-1998; 98US-0107466.
 PR 13-AUG-1999; 99US-0149010.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 DR WPI: 2000-339644/29.
 DR N-PSDB: AAD00206.
 XX
 XX New soluble CD39 polypeptides having apyrase activity, useful for
 PT inhibiting angiogenesis and treating unstable angina, myocardial
 PT infarction, stroke, coronary artery disease or injury -
 PS
 XX Claim 6a; Page 95-97; 122pp; English.
 XX
 XX The present sequence is a fusion construct, comprising the N-terminal
 CC amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39)
 CC region, that has apyrase activity. This results in high levels of
 CC solCD39 expression and activity in the transfected cells. Soluble CD39 is
 CC constructed by removing the N- and C-terminal transmembrane domains. It
 CC retains the capacity to metabolise ATP and ADP at relevant concentrations
 CC and the ability to block and reverse ADP-induced platelet activation and
 CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
 CC are useful for inhibiting platelet aggregation. It is useful for the treatment
 CC of unstable angina, myocardial infarction, stroke, coronary artery
 CC disease or injury, atherosclerosis, peripheral vascular occlusion,
 CC preclampsia, embolism, platelet-associated ischaemic disorders including

CC lung, coronary and cerebral ischaemia, thrombotic disorders including
 CC coronary, peripheral and cerebral artery thrombosis, intracardiac and
 CC venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
 CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also
 CC useful for preventing thrombus formation or reformation, occlusion,
 CC reocclusion, stenosis or restenosis of blood vessels or stroke.
 XX

SO Sequence 454 AA:

Query Match 78.1%; Score 75; DB 21; Length 454;
 Best Local Similarity 73.7%; Pred. No. 0.00011;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETGYALDGLGASTQ 19
 DB 180 ETNNQETFGALDGLGASTQ 198

RESULT 6

ID AAY70902 standard; Protein; 463 AA.

AC AAY70902;

DT 17-AUG-2000 (first entry)

DE Protein encoded by IgkappaSolCD39 construct.

XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; transient ischaemic attack; thrombus formation;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antiangiogenic; antiangiulant;
 KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;
 KW coronary ischaemia; vascular occlusion; IgkappaSolCD39 construct.
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Igkappa leader sequence"
 FT Cleavage-site 20..21
 FT Region 21..24
 FT /note= "Derived from IL-2"
 FT Region 25..32
 FT /note= "Derived from solCD39"
 FT Region 23..463
 FT /note= "soluble portion of CD39"
 XX WO200023094-A2.

PD 27-APR-2000.

PF 13-OCT-1999; 99WO-US23641.

XX 16-OCT-1998; 98US-0104585.

PR 06-NOV-1998; 98US-0107466.

XX 13-AUG-1999; 99US-0149010.

XX (IMMUNEX) IMMUNEX CORP.

PA (CORR) CORNELL RES FOUND INC.

PI Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI; 2000-339518/29.

XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,

PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides -
 XX Claim 6; Page 116-118; 118pp; English.

CC The present sequence is the protein encoded by IgkappaSolCD39 construct.
 CC This is used for transient expression of soluble(sol)CD39 in recombinant
 CC cells for determining enzymatic activity and platelet inhibitory activity
 CC for each protein product. SolCD39 is used in the treatment of unstable
 CC angina, myocardial infarction, stroke, coronary artery disease or injury,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
 CC platelet-associated ischaemic disorder including lung ischaemia, coronary
 CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
 CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke.
 XX

SO Sequence 463 AA:

Query Match 78.1%; Score 75; DB 21; Length 463;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETGYALDGLGASTQ 19

DB 189 ETNNQETFGALDGLGASTQ 207

RESULT 7

ID AAY70925 standard; Protein; 463 AA.

AC AAY70925;

DT 17-AUG-2000 (first entry)

DE Human soluble CD39 fusion protein construct, IgkappaSolCD39.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antiangiogenic; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KW cardiogenic; vasotrophic; thrombolytic; inhibitor; interleukin 2; IL2; Ig;
 KW immunoglobulin kappa.
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..20

FT /label= "Leader peptide"

FT /note= "Derived from human immunoglobulin Ig kappa"

FT Cleavage-site 20..21

FT /note= "Cleavage site of leader sequence"

FT Region 21..24

FT /note= "Residues derived from human interleukin 2 (IL2)"

FT Protein 23..463

FT /note= "Human soluble CD39 protein"

XX WO200023459-A1.

PD 27-APR-2000.

PF 13-OCT-1999; 99WO-US22955.

XX 16-OCT-1998; 98US-0104585.

PR 06-NOV-1998; 98US-0107466.

PR 13-AUG-1999; 99US-0149010.

XX (IMMUNEX CORP.

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI: 2000-339644/29.

DR New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiotensin and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury -
XX

PS Claim 6: Page 116-118; 122pp: English.

XX The present sequence is the fusion protein construct, IgkappaSolCD39.
CC This construct comprises of the leader peptide from human immunoglobulin
CC 1g kappa, linked to the soluble CD39 (solCD39) protein region by few
CC residues derived from human interleukin 2 (IL2). SolCD39 has apyrase
CC activity and is constructed by removing the N- and C-terminal
CC transmembrane domains. It retains the capacity to metabolise ATP and ADP
CC at relevant concentrations and the ability to block and reverse
CC ADP-induced platelet activation and recruitment, including platelet
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
CC myocardial infarction, coronary artery disease or injury, embolism,
CC atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
CC associated ischaemic disorders including lung, coronary and cerebral
CC ischaemia, thrombotic disorders including coronary, peripheral and
CC cerebral artery thrombosis, intracardiac and venous thrombosis,
CC cerebrovascular disease, deep venous thrombosis (DVT), pulmonary embolism (PE) and
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke.

XX Sequence 463 AA:

Query Match 78.1%; Score 75; DB 21; Length 463;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDPTGYGALDGGASTQ 19

DB 189 ETNNGEFGALDGGASTQ 207

RESULT 8

AAV70899 AAV70899 standard; Protein: 464 AA.

XX AAV70899;

XX 17-AUG-2000 (first entry)

DE Protein encoded by Trm 1 construct.

XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antilanginal; cardiac;
KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;
KW coronary ischaemia; vascular occlusion; pili2Trm1 variant.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers
FH Cleavage-site 24..25
FT Protein 26..464

note= "Soluble portion of CD39"

XX WO200023094-A2.

XX 27-APR-2000.

XX 13-OCT-1999; 99NO-US23641.

XX 16-OCT-1998; 98US-0104585.

XX 06-NOV-1998; 98US-0107466.

XX 13-AUG-1999; 99US-0149010.

XX (IMMUNEX CORP.

XX (CORR) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI: 2000-339518/29.

XX Example 11: Page 111-112; 118pp: English.

XX The present sequence is the protein encoded by Trm1 construct. pili2Trm1
XX variant was constructed by removing the human IL2 residues from solCD39
XX fusion construct. Fusion of 12 amino acids from the N-terminus of mature
XX human IL2 to the solCD39 coding region results in high levels of both
XX expression and activity in the supernatants of transfected cells. SolCD39
XX is used in the treatment of unstable angina, myocardial infarction,
XX stroke, coronary artery disease or injury, atherosclerosis, peripheral
XX vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
XX disorder including lung ischaemia, coronary ischaemia and cerebral
XX ischaemia, a thrombotic disorder including coronary artery thrombosis,
XX cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
XX thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
XX thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
XX Soluble CD39 is also useful for preventing thrombus formation or
XX reformation, occlusion, reocclusion, stenosis or restenosis of blood
XX vessels or stroke.

XX Sequence 464 AA:

Query Match 78.1%; Score 75; DB 21; Length 464;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDPTGYGALDGGASTQ 19

DB 190 ETNNGEFGALDGGASTQ 208

RESULT 9

AAV70922 AAV70922 standard; Protein: 464 AA.

XX AAV70922;

XX 17-AUG-2000 (first entry)

DE Human soluble CD39 fusion protein construct, pili2Trm1.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiotensin;
KW antilanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiac; vasotrophic; thrombolytic; inhibitor; interleukin 2; IL2.

CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
 CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
 CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
 CC thrombosis (DVT), pulmonary embolism (PE), transient ischemic attack.
 CC Soluble CD39 is also useful for preventing thrombus formation or
 CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
 CC vessels or stroke.

XX Sequence 474 AA:

Query Match 78.1%; Score 75; DB 21; Length 474;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETYGALDGGASTQ 19
 DB 200 ETNNQETFGALDGGASTQ 218

RESULT 13
 AAY70923

XX AAY70923 standard; Protein; 474 AA.

XX AC AAY70923;

XX DT 17-AUG-2000 (first entry)

XX DE Human soluble CD39 fusion protein construct, pIL2LTrm3.

XX Soluble CD39; solCD39; human: apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

XX OS Homo sapiens.
 XX Synthetic.

XX FH Key Location/Qualifiers
 XX FT Peptide 1..24

XX FT Cleavage-site /note= "Derived from human interleukin 2 (hIL2)"
 XX FT 24..25

XX FT Protein /note= "Cleavage site of leader sequence"
 XX FT 36..474
 XX /note= "Human soluble CD39 protein"

XX WO200023459-A1.

XX PD 27-APR-2000.

XX PF 13-OCT-1999; 99WO-US22955.

XX PR 16-OCT-1998; 98US-0104585.
 XX PR 06-NOV-1998; 98US-0107466.
 XX PR 13-AUG-1999; 99US-0149010.

XX PA (IMMV) IMMUNEX CORP.

XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX DR WPI: 2000-33964/29.

XX New soluble CD39 polypeptides having apyrase activity, useful for
 XX inhibiting angiogenesis and treating unstable angina, myocardial
 XX infarction, stroke, coronary artery disease or injury.
 XX Claim 6; Page 113-114; 122pp; English.

XX The present sequence is the fusion protein construct, pIL2LTrm3. This

CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
 CC and soluble CD39 (solCD39) protein region, having apyrase activity.

CC Soluble CD39 is constructed by removing the N- and C-terminal
 CC transmembrane domains. It retains the capacity to metabolize ATP and ADP
 CC at relevant concentrations and the ability to block and reverse
 CC ADP-induced platelet activation and recruitment, including platelet
 CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
 CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
 CC myocardial infarction, coronary artery disease or injury, embolism,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
 CC associated ischemic disorders including lung, coronary and cerebral
 CC ischaemia, thrombotic disorders including coronary, peripheral and
 CC cerebral artery thrombosis, intracardiac and venous thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
 CC transient ischemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke.

XX Sequence 474 AA:

Query Match 78.1%; Score 75; DB 21; Length 474;
 Best Local Similarity 73.7%; Pred. No. 0.00012;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETYGALDGGASTQ 19
 DB 200 ETNNQETFGALDGGASTQ 218

RESULT 14

XX AAY70888 standard; Protein; 476 AA.

XX AC AAY70888;

XX DT 17-AUG-2000 (first entry)

XX DE Protein encoded by CD39-L4-1 construct.

XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis;
 KW PE; pulmonary embolism; transient ischemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion.

XX OS Homo sapiens.
 XX Synthetic.

XX FH Key Location/Qualifiers
 XX FT Cleavage-site 20..21

XX FT Region /note= "Derived from CD39-L4"

XX FT 38..476
 XX /note= "Soluble portion of CD39"

XX WO200023094-A2.

XX PD 27-APR-2000.

XX PF 13-OCT-1999; 99WO-US23641.

XX PR 16-OCT-1998; 98US-0104585.
 XX PR 06-NOV-1998; 98US-0107466.
 XX PR 13-AUG-1999; 99US-0149010.

XX PA (IMMV) IMMUNEX CORP.
 XX (CORR) CORNELL RES FOUND INC.

BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Informa

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 30
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the in

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov

10

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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:36:22 : Search time 30 seconds
(without alignments)

18.635 Million cell updates/sec

Title: US-09-781-796b-7

Sequence: 1 KSDQETGYGALDLCGASTQ 19

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database:

1: Issued Patents AA: *
2: /cgn2_6/ptodata1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata1/1aa/6C.COMB.pep.*
6: /cgn2_6/ptodata1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
1	96	100.0	20	4	US-08-930-921-7	Sequence 7, Appl
2	82	85.4	16	4	US-08-930-921-8	Sequence 8, Appl
3	75	78.1	510	4	US-08-930-921-1	Sequence 1, Appl
4	64	66.7	405	4	US-09-608-285A-25	Sequence 25, Appl
5	64	66.7	405	4	US-09-370-265-25	Sequence 25, Appl
6	64	66.7	428	4	US-09-608-285A-3	Sequence 3, Appl
7	64	66.7	428	4	US-09-608-285A-5	Sequence 5, Appl
8	64	66.7	428	4	US-09-608-285A-7	Sequence 7, Appl
9	64	66.7	428	4	US-09-240-639-6	Sequence 6, Appl
10	64	66.7	428	4	US-09-240-639-9	Sequence 9, Appl
11	64	66.7	428	4	US-09-350-836B-3	Sequence 3, Appl
12	64	66.7	428	4	US-09-350-836B-5	Sequence 5, Appl
13	64	66.7	428	4	US-09-350-836B-7	Sequence 7, Appl
14	64	66.7	428	4	US-09-370-265-3	Sequence 3, Appl
15	64	66.7	428	4	US-09-370-265-5	Sequence 5, Appl
16	64	66.7	428	4	US-09-370-265-7	Sequence 7, Appl
17	64	66.7	428	4	US-09-240-639-8	Sequence 8, Appl
18	64	66.7	428	4	US-09-240-639-4	Sequence 4, Appl
19	64	66.7	428	4	US-09-129-112-2	Sequence 2, Appl
20	64	66.7	428	4	US-09-129-112-2	Sequence 2, Appl
21	64	66.7	428	4	US-09-608-285A-60	Sequence 60, Appl
22	64	66.7	428	4	US-09-608-285A-27	Sequence 27, Appl
23	64	66.7	428	4	US-09-370-265-27	Sequence 27, Appl
24	64	66.7	428	4	US-09-240-639-10	Sequence 10, Appl
25	64	66.7	428	4	US-09-129-112-15	Sequence 15, Appl
26	64	66.7	428	4	US-09-240-639-11	Sequence 11, Appl
27	64	66.7	428	4	US-09-129-112-9	Sequence 9, Appl

28	39	40.6	473	4	US-09-240-639-12	Sequence 12, Appl
29	38	39.6	31	4	US-08-905-223-410	Sequence 410, Appl
30	38	39.6	69	2	US-08-446-692-95	Sequence 95, Appl
31	38	39.6	69	2	US-08-488-351A-95	Sequence 95, Appl
32	38	39.6	332	2	US-08-637-763B-6	Sequence 6, Appl
33	38	39.6	332	2	US-09-170-354-6	Sequence 6, Appl
34	38	39.6	386	1	US-08-319-621A-14	Sequence 14, Appl
35	38	39.6	649	4	US-09-066-047-5	Sequence 5, Appl
36	38	39.6	678	5	PCR-US93-03027-3	Sequence 3, Appl
37	37	38.5	361	4	US-09-343-011B-2	Sequence 2, Appl
38	37	38.5	361	4	US-09-655-270A-21	Sequence 21, Appl
39	37	38.5	366	4	US-09-651-941-25	Sequence 25, Appl
40	37	38.5	366	4	US-09-955-597-25	Sequence 25, Appl
41	37	38.5	425	4	US-09-134-001C-5619	Sequence 5619, Appl
42	37	38.5	467	4	US-09-129-112-19	Sequence 19, Appl
43	36.5	38.0	1548	4	US-09-376-330-15	Sequence 15, Appl
44	36	37.5	40	2	US-08-926-842B-51	Sequence 51, Appl
45	36	37.5	123	2	US-08-665-202-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-930-921-7
Sequence 7, Application US/08930921B
Patent No. 6287837
GENERAL INFORMATION:
APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SEVIGNY, Jean
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
CURRENT FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: US/08/930,921B
EARLIER FILING DATE: 1996-04-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE: Unknown
OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-7
Query Match 100.0%; Score 96; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2; le-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSDQETGYGALDLCGASTQ 19
DB 1 KSDQETGYGALDLCGASTQ 19
RESULT 2
US-08-930-921-8
Sequence 8, Application US/08930921B
Patent No. 6287837
GENERAL INFORMATION:
APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SEVIGNY, Jean
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
CURRENT FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: PCT/CA96/00223
EARLIER FILING DATE: 1996-04-10
NUMBER OF SEQ ID NOS: 8

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SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-8

Query Match
Best Local Similarity 85.4%; Score 82; DB 4; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSDTQETGALDGGASTQ 16
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RESULT 3
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; Sequence 1, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THERMOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; EARLIER FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: PCT/CA96/00223
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-1

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Best Local Similarity 78.1%; Score 75; DB 4; Length 510;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETGALDGGASTQ 19
DB 202 ETNDETGALDGGASTQ 220

RESULT 4
US-09-608-285A-25
; Sequence 25, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Muleto, George
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09

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; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-25

Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 405;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 QETGALDGGASTQ 19
DB 192 QETGALDGGASTQ 206

RESULT 5
US-09-370-265-25
; Sequence 25, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Muleto, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; EARLIER FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
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; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-25

Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 405;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 QETGALDGGASTQ 19
DB 192 QETGALDGGASTQ 206

RESULT 6
US-09-608-285A-3
; Sequence 3, Application US/09608285A

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Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-3

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 QETYGALDGGASTQ 19
||| | ||||| |||
Db 192 QETVGTLDGGASTQ 206

RESULT 7
US-09-608-285A-5
Sequence 5, Application US/09608285A
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-5

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 QETYGALDGGASTQ 19
||| | ||||| |||
Db 192 QETVGTLDGGASTQ 206

RESULT 8
US-09-608-285A-7
Sequence 7, Application US/09608285A
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-7

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 QETYGALDGGASTQ 19
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Db 192 QETVGTLDGGASTQ 206

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RESULT 9
US-09-240-639-6
; Sequence 6, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-6

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206

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RESULT 10
US-09-240-639-9
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-9

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206

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RESULT 11
US-09-350-836B-3
; Sequence 3, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19

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; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-3

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206

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RESULT 12
US-09-350-836B-5
; Sequence 5, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-5

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Query Match
Best Local Similarity 66.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 5 QETYGALDLGASTQ 19
DB 192 QETVGTLDLGASTQ 206

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RESULT 13
US-09-350-836B-7
; Sequence 7, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447

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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-350-836B-7

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Query Match      66.7% Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY      5 QETYGALDLGASTQ 19
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Db      192 QETVGTLDLGASTQ 206

```

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RESULT 14
US-09-370-265-3
; Sequence 3, Application US/09370265
; Patent No. 644771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-370-265-3

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Query Match      66.7% Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      5 QETYGALDLGASTQ 19
      ||| | ||||| |||
Db      192 QETVGTLDLGASTQ 206

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RESULT 15
US-09-370-265-5
; Sequence 5, Application US/09370265
; Patent No. 644771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

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; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-370-265-5

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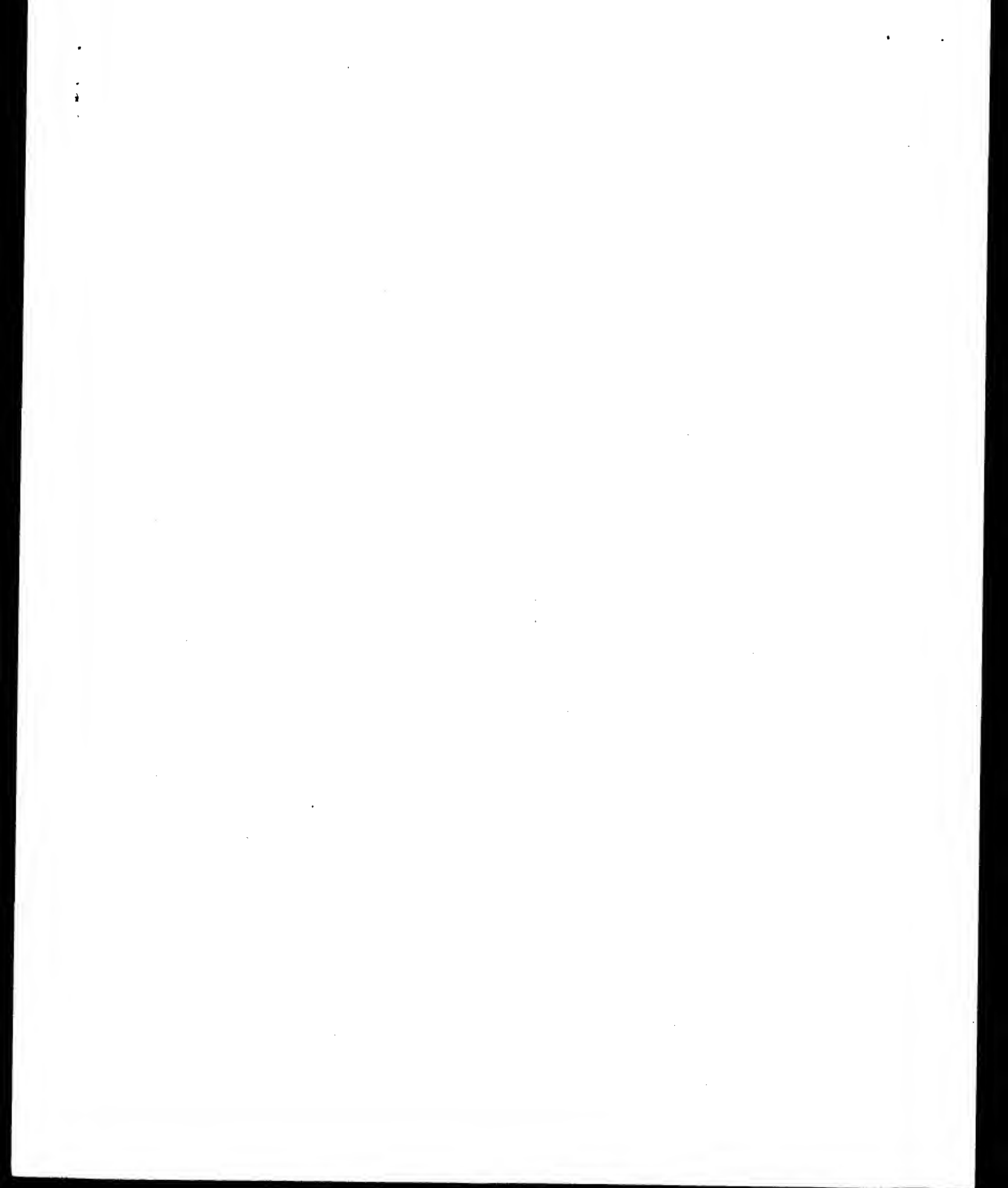
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Best Local Similarity 86.7%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      5 QETYGALDLGASTQ 19
      ||| | ||||| |||
Db      192 QETVGTLDLGASTQ 206

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Job time : 32 secs

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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:39:47 (Search time 12 seconds
(without alignments)
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Title: US-09-781-796b-7
Perfect score: 96
Sequence: 1 KSDQETGYGALDGGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications, AA:*

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- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB pep:*
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- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB pep:*
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- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEM_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	78.1	439	US-09-374-586-2	Sequence 2, Appli
2	75	78.1	454	US-09-835-147-6	Sequence 6, Appli
3	75	78.1	463	US-09-835-147-30	Sequence 30, Appli
4	75	78.1	464	US-09-835-147-27	Sequence 27, Appli
5	75	78.1	473	US-09-835-147-29	Sequence 29, Appli
6	75	78.1	474	US-09-835-147-28	Sequence 28, Appli
7	75	78.1	476	US-09-835-147-3	Sequence 3, Appli
8	75	78.1	476	US-09-835-147-4	Sequence 4, Appli
9	75	78.1	478	US-09-835-147-8	Sequence 8, Appli
10	75	78.1	487	US-09-835-147-26	Sequence 26, Appli
11	75	78.1	502	US-10-092-063-38	Sequence 38, Appli
12	75	78.1	510	US-09-835-147-2	Sequence 2, Appli
13	75	78.1	510	US-09-374-586-1	Sequence 1, Appli
14	64	66.7	405	US-10-092-063-25	Sequence 25, Appli
15	64	66.7	428	US-10-092-063-3	Sequence 3, Appli
16	64	66.7	428	US-10-092-063-5	Sequence 5, Appli
17	64	66.7	428	US-10-092-063-7	Sequence 7, Appli
18	64	66.7	428	US-10-091-085-3	Sequence 3, Appli
19	64	66.7	428	US-10-091-085-5	Sequence 5, Appli

ALIGNMENTS

20	64	66.7	428	12	US-10-091-085-7	Sequence 7, Appli
21	64	66.7	465	9	US-10-092-063-39	Sequence 39, Appli
22	62	64.6	529	10	US-09-923-304-4	Sequence 4, Appli
23	60	62.5	330	10	US-09-925-299-876	Sequence 876, App
24	52	54.2	458	9	US-10-174-590-496	Sequence 496, App
25	52	54.2	458	9	US-10-176-758-496	Sequence 496, App
26	52	54.2	458	9	US-10-175-737-496	Sequence 496, App
27	52	54.2	458	9	US-10-173-706-496	Sequence 496, App
28	52	54.2	458	9	US-10-175-738-496	Sequence 496, App
29	52	54.2	458	9	US-10-173-752-496	Sequence 496, App
30	52	54.2	458	9	US-10-176-482-496	Sequence 496, App
31	52	54.2	458	9	US-10-176-757-496	Sequence 496, App
32	52	54.2	458	9	US-10-175-913-496	Sequence 496, App
33	52	54.2	458	9	US-10-180-553-496	Sequence 496, App
34	52	54.2	458	9	US-10-180-557-496	Sequence 496, App
35	52	54.2	458	9	US-10-173-700-496	Sequence 496, App
36	52	54.2	458	9	US-10-174-572-496	Sequence 496, App
37	52	54.2	458	9	US-10-174-579-496	Sequence 496, App
38	52	54.2	458	9	US-10-174-582-496	Sequence 496, App
39	52	54.2	458	9	US-10-174-588-496	Sequence 496, App
40	52	54.2	458	9	US-10-175-739-496	Sequence 496, App
41	52	54.2	458	9	US-10-175-740-496	Sequence 496, App
42	52	54.2	458	9	US-10-175-743-496	Sequence 496, App
43	52	54.2	458	9	US-10-176-488-496	Sequence 496, App
44	52	54.2	458	9	US-10-176-492-496	Sequence 496, App
45	52	54.2	458	9	US-10-176-747-496	Sequence 496, App

RESULT 1
US-09-374-586-2
Sequence 2, Application US/09374586
Patent No. US20020138858A1
GENERAL INFORMATION:
APPLICANT: Plinsky, David J.
TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374,586
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 73.1% Score 75; DB 10; Length 439;

Best Local Similarity 73.7% Pred. No. 4.2e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETGYGALDGGASTQ 19
Db 165 ETNDETGYGALDGGASTQ 183
RESULT 2
US-09-835-147-6
Sequence 6, Application US/09835147
Patent No. US2002002277A1
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpe, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585

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; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

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Query Match      78.1% Score 75; DB 10; Length 454;
Best Local Similarity 73.7% Pred. No. 4.4e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY      1 KSDQETFGALDLCGASTQ 19
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Db      180 ETNNQETFGALDLCGASTQ 198

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RESULT 3
US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

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Query Match      78.1% Score 75; DB 10; Length 463;
Best Local Similarity 73.7% Pred. No. 4.5e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 KSDQETFGALDLCGASTQ 19
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Db      189 ETNNQETFGALDLCGASTQ 207

```

```

RESULT 4
US-09-835-147-27
; Sequence 27, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:

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; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-27

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```

Query Match      78.1% Score 75; DB 10; Length 464;
Best Local Similarity 73.7% Pred. No. 4.5e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 KSDQETFGALDLCGASTQ 19
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Db      190 ETNNQETFGALDLCGASTQ 208

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RESULT 5
US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

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Query Match      78.1% Score 75; DB 10; Length 473;
Best Local Similarity 73.7% Pred. No. 4.6e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY      1 KSDQETFGALDLCGASTQ 19

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Db 199 ETNNQETFGALDLAGASTQ 217

RESULT 6

US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
US-09-835-147-28

Query Match 78.1%; Score 75; DB 10; Length 474;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETFGALDLAGASTQ 19
Db 200 ETNNQETFGALDLAGASTQ 218

RESULT 7

US-09-835-147-3
; Sequence 3, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-3

Query Match

78.1%; Score 75; DB 10; Length 476;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETFGALDLAGASTQ 19
Db 202 ETNNQETFGALDLAGASTQ 220

RESULT 8

US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

Query Match 78.1%; Score 75; DB 10; Length 476;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETFGALDLAGASTQ 19
Db 202 ETNNQETFGALDLAGASTQ 220

RESULT 9

US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466

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; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
US-09-835-147-8
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Query Match
Best Local Similarity 78.1%; Score 75; DB 10; Length 478;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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DB 204 ETNNQETFGALDUGASTQ 222
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; Sequence 26, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
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; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
US-09-835-147-26
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Query Match
Best Local Similarity 78.1%; Score 75; DB 10; Length 487;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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DB 213 ETNNQETFGALDUGASTQ 231
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RESULT 11
US-10-092-063-38
; Sequence 38, Application US/10092063
; Patent No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Malero, Julio
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; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
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; ORGANISM: Homo sapiens
US-10-092-063-38
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DB 202 ETNNQETFGALDUGASTQ 220
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RESULT 12
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; Sequence 2, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
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US-09-835-147-2
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Best Local Similarity 78.1%; Score 75; DB 10; Length 510;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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DB 202 ETNNQETFGALDUGASTQ 220
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RESULT 13
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; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Plinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; FILE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.1
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; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match      78.1%; Score 75; DB 10; Length 510;
Best Local Similarity 73.7%; Pred. No. 5e-05;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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DB      202 ETNNOETFGALDLGASTQ 220

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; Sequence 25, Application US/10092063
; Patent No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-25

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DB      192 QETVGTLDLGASTQ 206

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; Sequence 3, Application US/10092063
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; Patent No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
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; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-3

Query Match      66.7%; Score 64; DB 9; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0029;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 QETYGALDLGASTQ 19
DB      192 QETVGTLDLGASTQ 206

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Job time : 13 secs
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OM protein - protein search, using SW model

Run on: February 11, 2003, 18:37:47 ; Search time 354 Seconds
(without alignments)
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Title: US-09-781-796b-7

Perfect score: 96
Sequence: 1 KSDQETGALDLSASTQ 19

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 4569144

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	82	85.4	16	21	US-09-781-796b-8
3	75	78.1	276	19	US-09-558-630A-30
4	75	78.1	439	1	PCT-US00-22060-2
5	75	78.1	439	17	US-09-374-586-2
6	75	78.1	454	1	PCT-US99-22935-6

7	75	78.1	454	22	US-09-807-660A-6	Sequence 6, Appl
8	75	78.1 <td>454</td> <td>22<th>US-09-835-147-6</th><th>Sequence 6, Appl</th></td>	454	22 <th>US-09-835-147-6</th> <th>Sequence 6, Appl</th>	US-09-835-147-6	Sequence 6, Appl
9	75	78.1 <td>453</td> <td>1<th>PCT-US99-22955-30</th><th>Sequence 30, Appl</th></td>	453	1 <th>PCT-US99-22955-30</th> <th>Sequence 30, Appl</th>	PCT-US99-22955-30	Sequence 30, Appl
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11	75	78.1 <td>463</td> <td>22<th>US-09-835-147-30</th><th>Sequence 27, Appl</th></td>	463	22 <th>US-09-835-147-30</th> <th>Sequence 27, Appl</th>	US-09-835-147-30	Sequence 27, Appl
12	75	78.1 <td>464</td> <td>1<th>PCT-US99-22955-27</th><th>Sequence 27, Appl</th></td>	464	1 <th>PCT-US99-22955-27</th> <th>Sequence 27, Appl</th>	PCT-US99-22955-27	Sequence 27, Appl
13	75	78.1 <td>464</td> <td>22<th>US-09-807-660A-27</th><th>Sequence 27, Appl</th></td>	464	22 <th>US-09-807-660A-27</th> <th>Sequence 27, Appl</th>	US-09-807-660A-27	Sequence 27, Appl
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16	75	78.1 <td>473</td> <td>22<th>US-09-807-660A-29</th><th>Sequence 29, Appl</th></td>	473	22 <th>US-09-807-660A-29</th> <th>Sequence 29, Appl</th>	US-09-807-660A-29	Sequence 29, Appl
17	75	78.1 <td>473</td> <td>22<th>US-09-835-147-29</th><th>Sequence 28, Appl</th></td>	473	22 <th>US-09-835-147-29</th> <th>Sequence 28, Appl</th>	US-09-835-147-29	Sequence 28, Appl
18	75	78.1 <td>474</td> <td>1<th>PCT-US99-22955-28</th><th>Sequence 28, Appl</th></td>	474	1 <th>PCT-US99-22955-28</th> <th>Sequence 28, Appl</th>	PCT-US99-22955-28	Sequence 28, Appl
19	75	78.1 <td>474</td> <td>22<th>US-09-807-660A-28</th><th>Sequence 28, Appl</th></td>	474	22 <th>US-09-807-660A-28</th> <th>Sequence 28, Appl</th>	US-09-807-660A-28	Sequence 28, Appl
20	75	78.1 <td>474</td> <td>22<th>US-09-835-147-28</th><th>Sequence 3, Appl</th></td>	474	22 <th>US-09-835-147-28</th> <th>Sequence 3, Appl</th>	US-09-835-147-28	Sequence 3, Appl
21	75	78.1 <td>476</td> <td>1<th>PCT-US99-22955-3</th><th>Sequence 3, Appl</th></td>	476	1 <th>PCT-US99-22955-3</th> <th>Sequence 3, Appl</th>	PCT-US99-22955-3	Sequence 3, Appl
22	75	78.1 <td>476</td> <td>1<th>PCT-US99-22955-4</th><th>Sequence 4, Appl</th></td>	476	1 <th>PCT-US99-22955-4</th> <th>Sequence 4, Appl</th>	PCT-US99-22955-4	Sequence 4, Appl
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24	75	78.1 <td>476</td> <td>22<th>US-09-807-660A-4</th><th>Sequence 4, Appl</th></td>	476	22 <th>US-09-807-660A-4</th> <th>Sequence 4, Appl</th>	US-09-807-660A-4	Sequence 4, Appl
25	75	78.1 <td>476</td> <td>22<th>US-09-835-147-3</th><th>Sequence 3, Appl</th></td>	476	22 <th>US-09-835-147-3</th> <th>Sequence 3, Appl</th>	US-09-835-147-3	Sequence 3, Appl
26	75	78.1 <td>476</td> <td>22<th>US-09-835-147-3</th><th>Sequence 4, Appl</th></td>	476	22 <th>US-09-835-147-3</th> <th>Sequence 4, Appl</th>	US-09-835-147-3	Sequence 4, Appl
27	75	78.1 <td>478</td> <td>1<th>PCT-US99-22955-8</th><th>Sequence 8, Appl</th></td>	478	1 <th>PCT-US99-22955-8</th> <th>Sequence 8, Appl</th>	PCT-US99-22955-8	Sequence 8, Appl
28	75	78.1 <td>478</td> <td>22<th>US-09-807-660A-8</th><th>Sequence 8, Appl</th></td>	478	22 <th>US-09-807-660A-8</th> <th>Sequence 8, Appl</th>	US-09-807-660A-8	Sequence 8, Appl
29	75	78.1 <td>478</td> <td>22<th>US-09-835-147-8</th><th>Sequence 26, Appl</th></td>	478	22 <th>US-09-835-147-8</th> <th>Sequence 26, Appl</th>	US-09-835-147-8	Sequence 26, Appl
30	75	78.1 <td>487</td> <td>1<th>PCT-US99-22955-26</th><th>Sequence 26, Appl</th></td>	487	1 <th>PCT-US99-22955-26</th> <th>Sequence 26, Appl</th>	PCT-US99-22955-26	Sequence 26, Appl
31	75	78.1 <td>487</td> <td>22<th>US-09-807-660A-26</th><th>Sequence 26, Appl</th></td>	487	22 <th>US-09-807-660A-26</th> <th>Sequence 26, Appl</th>	US-09-807-660A-26	Sequence 26, Appl
32	75	78.1 <td>487</td> <td>22<th>US-09-835-147-26</th><th>Sequence 26, Appl</th></td>	487	22 <th>US-09-835-147-26</th> <th>Sequence 26, Appl</th>	US-09-835-147-26	Sequence 26, Appl
33	75	78.1 <td>502</td> <td>17<th>US-09-370-625A-38</th><th>Sequence 55, Appl</th></td>	502	17 <th>US-09-370-625A-38</th> <th>Sequence 55, Appl</th>	US-09-370-625A-38	Sequence 55, Appl
34	75	78.1 <td>502</td> <td>19<th>US-09-557-800C-55</th><th>Sequence 38, Appl</th></td>	502	19 <th>US-09-557-800C-55</th> <th>Sequence 38, Appl</th>	US-09-557-800C-55	Sequence 38, Appl
35	75	78.1 <td>502</td> <td>24<th>US-10-092-063-38</th><th>Sequence 1, Appl</th></td>	502	24 <th>US-10-092-063-38</th> <th>Sequence 1, Appl</th>	US-10-092-063-38	Sequence 1, Appl
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44	69	71.9	120	22 <th>US-09-834-366-17027</th> <th>Sequence 17027, A</th>	US-09-834-366-17027	Sequence 17027, A

ALIGNMENTS

RESULT 1
US-09-781-796b-7
Sequence 7, Application US/09781796b
GENERAL INFORMATION:
APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SVIGNY, Jean
APPLICANT: BACH, Fritz H.
TITLE OF INVENTION: ROBSON, Simon
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
FILE REFERENCE: 920333.90019
CURRENT APPLICATION NUMBER: US/09/781.796b
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 08/419.204
PRIOR FILING DATE: 1995-04-10
PRIOR APPLICATION NUMBER: CA56/00223
PRIOR FILING DATE: 1996-04-10
PRIOR APPLICATION NUMBER: 08/930.921
PRIOR FILING DATE: 1998-02-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 19
TYPE: PRT
ORGANISM: Porcine
US-09-781-796b-7
Query Match 100.0%, score 96; DB 21; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLCGASTQ 19
Db 1 KSDTQETYGALDLCGASTQ 19

RESULT 2

US-09-781-796b-8
Sequence 8, Application US/09781796b
GENERAL INFORMATION:
APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SVIGNY, Jean
APPLICANT: BACH, Fritz H.
APPLICANT: ROBSON, Simon
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
FILE REFERENCE: 920333.90019
CURRENT APPLICATION NUMBER: US/09/781.796b
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 08/419,204
PRIOR FILING DATE: 1995-04-10
PRIOR APPLICATION NUMBER: CA96/00223
PRIOR FILING DATE: 1996-04-10
PRIOR APPLICATION NUMBER: 08/930,921
PRIOR FILING DATE: 1998-02-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 8
LENGTH: 16
TYPE: PRT
ORGANISM: Human and bovine
US-09-781-796b-8

Query Match 85.4%; Score 82; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLCGA 16
Db 1 KSDTQETYGALDLCGA 16

RESULT 3

US-09-558-630A-30
Sequence 30, Application US/09558630A
GENERAL INFORMATION:
APPLICANT: MINTZ, Lia et al.
TITLE OF INVENTION: ALTERNATIVE SPLICE VARIANTS
FILE REFERENCE: 2786-0150P
CURRENT APPLICATION NUMBER: US/09/558.630A
CURRENT FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentln Version 3.1
SEQ ID NO 30
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-558-630A-30

Query Match 78.1%; Score 75; DB 19; Length 276;
Best Local Similarity 73.7%; Pred. No. 0.00043;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLCGASTQ 19
Db 202 ETNNOETFGALDLCGASTQ 220

RESULT 4
PCT-US00-22060-2

Sequence 2, Application PC/TUS0022060
GENERAL INFORMATION:
APPLICANT: PINSKY, David J.
TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
TITLE OF INVENTION: ISCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: PCT/US00/22060
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-22060-2

Query Match 78.1%; Score 75; DB 1; Length 439;
Best Local Similarity 73.7%; Pred. No. 0.00076;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLCGASTQ 19
Db 165 ETNNOETFGALDLCGASTQ 183

RESULT 5

US-09-374-586-2
Sequence 2, Application US/09374586
GENERAL INFORMATION:
APPLICANT: PINSKY, David J.
TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
TITLE OF INVENTION: ISCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374.586
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 78.1%; Score 75; DB 17; Length 439;
Best Local Similarity 73.7%; Pred. No. 0.00076;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLCGASTQ 19
Db 165 ETNNOETFGALDLCGASTQ 183

RESULT 6

PCT-US99-22955-6
Sequence 6, Application PC/TUS9922955
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
APPLICANT: Immunex Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-WO
CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
EARLIER FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/149,010
EARLIER FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
PCT-US99-22955-6

Query Match 78.1%; Score 75; DB 1; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETYGALDLCGASTQ 19
DB 180 ETNNQETFGALDLCGASTQ 198

RESULT 7
US-09-807-660A-6
Sequence 6, Application US/09807660A

GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Marcus, Aaron J.
APPLICANT: Immunex Corporation
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
TITLE OF INVENTION: Recruitment
FILE REFERENCE: 23,495 PCT
CURRENT APPLICATION NUMBER: US/09/807,660A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: Construct of human CD39
US-09-807-660A-6

Query Match 78.1%; Score 75; DB 22; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETYGALDLCGASTQ 19
DB 180 ETNNQETFGALDLCGASTQ 198

RESULT 8
US-09-835-147-6
Sequence 6, Application US/09835147
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: Construct of human CD39
US-09-835-147-6

Query Match 78.1%; Score 75; DB 22; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETYGALDLCGASTQ 19
DB 180 ETNNQETFGALDLCGASTQ 198

RESULT 9
PCT-US99-22955-30
Sequence 30, Application PC/TUS9922955
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
APPLICANT: Immunex Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
TITLE OF INVENTION: Recruitment
FILE REFERENCE: 2879-WO
CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 30
LENGTH: 463
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: Construct of human CD39
PCT-US99-22955-30

Query Match 78.1%; Score 75; DB 1; Length 463;
Best Local Similarity 73.7%; Pred. No. 0.00081;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDQETYGALDLCGASTQ 19
DB 189 ETNNQETFGALDLCGASTQ 207

RESULT 10
US-09-807-660A-30
Sequence 30, Application US/09807660A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Marcus, Aaron J.
APPLICANT: Immunex Corporation
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
TITLE OF INVENTION: Recruitment
FILE REFERENCE: 23,495 PCT

RESULT 14
US-09-835-147-27

Sequence 27, Application US/09835147

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Price, Virginia L.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-10-16

PRIOR APPLICATION NUMBER: US 60/107,466

PRIOR FILING DATE: 1998-11-06

PRIOR APPLICATION NUMBER: US 60/149,010

PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955

PRIOR FILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 27

LENGTH: 464

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion

OTHER INFORMATION: construct of human CD39

US-09-835-147-27

Query Match 78.1%; Score 75; DB 22; Length 464;

Best Local Similarity 73.7%; Pred. No. 0.00081;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETYGALDGGASTQ 19

DB 190 ETNNEETFGALDGGASTQ 208

RESULT 15

PCT-US99-22955-29

Sequence 29, Application PC/7US9922955

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Price, Virginia L.

APPLICANT: Gimpel, Steven D.

APPLICANT: Immunex Corporation

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: PCT/US99/22955

CURRENT FILING DATE: 1999-10-13

EARLIER APPLICATION NUMBER: US 60/104,585

EARLIER FILING DATE: 1998-10-16

EARLIER APPLICATION NUMBER: US 60/107,466

EARLIER FILING DATE: 1998-11-06

EARLIER APPLICATION NUMBER: US 60/149,010

EARLIER FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 473

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion

OTHER INFORMATION: construct of human CD39

PCT-US99-22955-29

Query Match 78.1%; Score 75; DB 1; Length 473;

Best Local Similarity 73.7%; Pred. No. 0.00083;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETYGALDGGASTQ 19

DB 199 ETNNEETFGALDGGASTQ 217

Search completed: February 11, 2003, 18:46:40
Job time : 355 secs

11

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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:38:07 ; Search time 19 Seconds
(without alignments)
83.231 Million cell updates/sec

Title: US-09-781-796b-7
Perfect score: 96
Sequence: 1 KSDQETFGALDLCASQ 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 420401 seqs, 83231269 residues

Total number of hits satisfying chosen parameters: 420401

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
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4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	78.1	276	5	US-09-724-676-59001
2	75	78.1	276	5	US-09-724-676A-59001
3	75	78.1	283	5	US-09-724-676-59000
4	75	78.1	283	5	US-09-724-676A-59000
5	75	78.1	439	6	US-10-049-420-2
6	75	78.1	434	5	US-09-835-147A-6
7	75	78.1	463	5	US-09-835-147A-30
8	75	78.1	464	5	US-09-835-147A-27
9	75	78.1	473	5	US-09-835-147A-29
10	75	78.1	474	5	US-09-835-147A-28
11	75	78.1	476	5	US-09-835-147A-3
12	75	78.1	478	5	US-09-835-147A-4
13	75	78.1	487	5	US-09-835-147A-8
14	75	78.1	487	5	US-09-835-147A-26
15	75	78.1	510	5	US-09-835-147A-2
16	75	78.1	510	6	US-10-049-420-1
17	75	78.1	517	5	US-09-724-676-58998
18	75	78.1	517	5	US-09-724-676-58999
19	75	78.1	517	5	US-09-724-676A-58998
20	75	78.1	517	5	US-09-724-676A-58999
21	58	60.4	701	6	US-10-310-154-534
22	52	54.2	458	1	PCT-US02-40161-16
23	52	54.2	458	1	PCT-US02-40161-30
24	52	54.2	458	6	US-10-125-923A-496
25	52	54.2	458	6	US-10-205-892-496
26	52	54.2	458	6	US-10-174-575-496

27	52	54.2	458	6	US-10-174-575A-496	Sequence 496, App
28	52	54.2	458	6	US-10-187-735-496	Sequence 496, App
29	52	54.2	458	6	US-10-187-749-496	Sequence 496, App
30	52	54.2	458	6	US-10-199-672-496	Sequence 496, App
31	47	49.0	435	5	US-09-724-676-76017	Sequence 76017, A
32	47	49.0	435	5	US-09-724-676A-76017	Sequence 76019, A
33	47	49.0	451	5	US-09-724-676A-76019	Sequence 76019, A
34	47	49.0	451	5	US-09-724-676A-76016	Sequence 76016, A
35	47	49.0	594	5	US-09-724-676A-76018	Sequence 76018, A
36	47	49.0	602	5	US-09-724-676A-76018	Sequence 59094, A
37	47	49.0	602	5	US-09-724-676-59094	Sequence 59085, A
38	47	49.0	602	5	US-09-724-676-59085	Sequence 59086, A
39	46	47.9	402	5	US-09-724-676-59087	Sequence 59087, A
40	46	47.9	402	5	US-09-724-676-59088	Sequence 59088, A
41	46	47.9	402	5	US-09-724-676-59085	Sequence 59085, A
42	46	47.9	402	5	US-09-724-676-59088	Sequence 59088, A
43	46	47.9	402	5	US-09-724-676-59085	Sequence 59085, A
44	46	47.9	402	5	US-09-724-676-59088	Sequence 59088, A
45	46	47.9	402	5	US-09-724-676A-59085	Sequence 59085, A

ALIGNMENTS

RESULT 1
US-09-724-676-59001
Sequence 59001, Application US/09724676
GENERAL INFORMATION:
APPLICANT: CompuGen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 CompuGen
CURRENT APPLICATION NUMBER: US/09724, 676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59001
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-59001
Query Match 78.1%; Score 75; DB 5; Length 276;
Best Local Similarity 73.7%; Pred. No. 0.00013;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETFGALDLCASQ 19
DB 202 ETNNOETFGALDLCASQ 220
RESULT 2
US-09-724-676A-59001
Sequence 59001, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: CompuGen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 CompuGen
CURRENT APPLICATION NUMBER: US/09724, 676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59001
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-59001
Query Match 78.1%; Score 75; DB 5; Length 276;
Best Local Similarity 73.7%; Pred. No. 0.00013;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSDQETFGALDLCASQ 19
DB 202 ETNNOETFGALDLCASQ 220

Db 202 ETNNOETFGALDGGASTQ 220

RESULT 3

US-09-724-676-59000
Sequence 59000, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59000
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-59000

Query Match

Best Local Similarity 78.1%; Score 75; DB 5; Length 283;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 209 ETNNOETFGALDGGASTQ 227

RESULT 4

US-09-724-676A-59000
Sequence 59000, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59000
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-59000

Query Match

Best Local Similarity 78.1%; Score 75; DB 5; Length 283;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 209 ETNNOETFGALDGGASTQ 227

RESULT 5

US-10-049-420-2
Sequence 2, Application US/10049420
GENERAL INFORMATION:
APPLICANT: Pinsky, David J.
TITLE OF INVENTION: CD39/EC20-ADPASE AS A TREATMENT FOR THROMBOTIC AND
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/10/049,420
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US/09/374,586
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens

US-10-049-420-2

Query Match 78.1%; Score 75; DB 6; Length 439;
Best Local Similarity 73.7%; Pred. No. 0.00021;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 165 ETNNOETFGALDGGASTQ 183

RESULT 6

US-09-835-147A-6
Sequence 6, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-6

Query Match 78.1%; Score 75; DB 5; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00022;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETFGALDGGASTQ 19
Db 180 ETNNOETFGALDGGASTQ 198

RESULT 7

US-09-835-147A-30
Sequence 30, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30

LENGTH: 463
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-30

Query Match 78.1%; Score 75; DB 5; Length 463;
Best Local Similarity 73.7%; Pred. No. 0.00022;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 189 ETNNOETFGALDLCGASTQ 207

RESULT 8
US-09-835-147A-27
Sequence 27, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpe, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 464
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-27

Query Match 78.1%; Score 75; DB 5; Length 464;
Best Local Similarity 73.7%; Pred. No. 0.00022;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 190 ETNNOETFGALDLCGASTQ 208

RESULT 9
US-09-835-147A-29
Sequence 29, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpe, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-29

Query Match 78.1%; Score 75; DB 5; Length 473;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 199 ETNNOETFGALDLCGASTQ 217

RESULT 10
US-09-835-147A-28
Sequence 28, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpe, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 474
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-28

Query Match 78.1%; Score 75; DB 5; Length 474;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSDTQETFGALDLCGASTQ 19
DB 200 ETNNOETFGALDLCGASTQ 218

RESULT 11
US-09-835-147A-3
Sequence 3, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpe, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 476
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-3

Query Match 78.1%; Score 75; DB 5; Length 476;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETFGALDGGASTQ 19
::: |||:|||||
DB 202 ETNNOETFGALDGGASTQ 220

RESULT 12
US-09-835-147A-4
Sequence 4, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 476
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
NAME/KEY: MISC_FEATURE
LOCATION: (39)..(39)
OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147A-4

Query Match 78.1%; Score 75; DB 5; Length 476;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSDQETFGALDGGASTQ 19
::: |||:|||||
DB 202 ETNNOETFGALDGGASTQ 220

RESULT 13
US-09-835-147A-8
Sequence 8, Application US/09835147A
GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 478
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-8

Query Match 78.1%; Score 75; DB 5; Length 478;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDQETFGALDGGASTQ 19
::: |||:|||||
DB 204 ETNNOETFGALDGGASTQ 222

RESULT 14
US-09-835-147A-26
Sequence 26, Application US/09835147A
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147A
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 487
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion construct of human CD39
US-09-835-147A-26

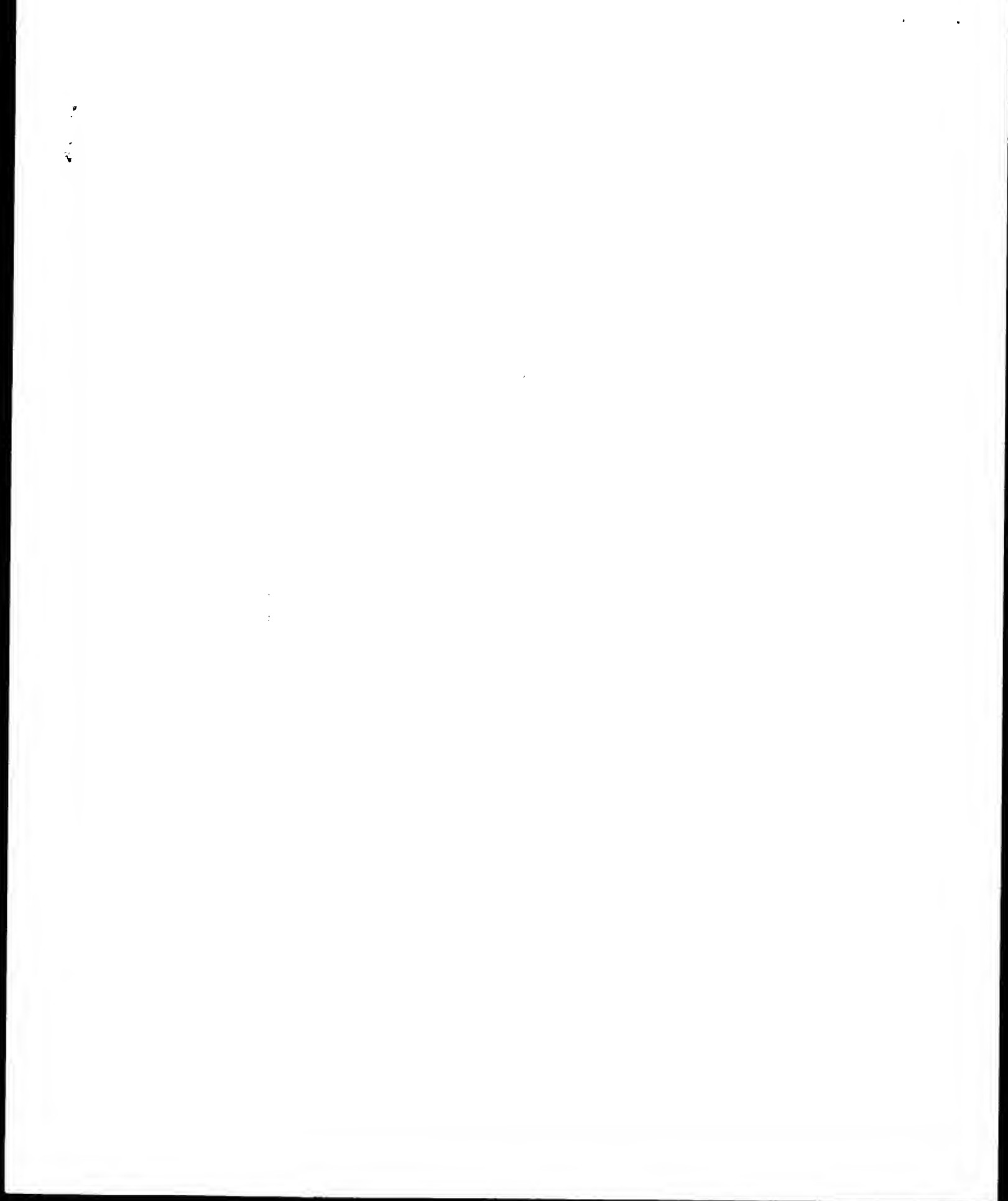
Query Match 78.1%; Score 75; DB 5; Length 487;
Best Local Similarity 73.7%; Pred. No. 0.00023;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSDQETFGALDGGASTQ 19
::: |||:|||||
DB 213 ETNNOETFGALDGGASTQ 231

```
RESULT 15
US-09-835-147A-2
; Sequence 2, Application US/09835147A
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimbel, Steven D.
; TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-147A-2

Query Match          78.1%; Score 75; DB 5; Length 510;
Best Local Similarity 73.7%; Pred. No. 0.00024;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSDTQETYGALDLGASTQ 19
      :: |||:|||||
Db      202 ETNQETFGALDLGASTQ 220
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Search completed: February 11, 2003, 18:47:06
Job time : 20 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:35:31 ; search time 16 Seconds
(without alignments)

114.160 Million cell updates/sec

Title: US-09-781-796b-7

Perfect score: 96
Sequence: 1 KSDTQETYGALDLGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	78.1	510	2	156242
2	62	64.6	44	2	S63501
3	53	55.2	1052	2	T04439
4	52	54.2	630	2	S50463
5	51	53.1	556	2	T39109
6	50	52.1	557	2	T16696
7	49	51.0	483	2	D86276
8	47	49.0	124	1	PAD02
9	46.5	48.4	572	2	T40856
10	44	45.8	263	2	C70741
11	44	45.8	377	2	S56505
12	44	45.8	405	2	E86726
13	44	45.8	455	2	S48859
14	44	45.8	516	2	G84442
15	44	45.8	925	2	S27920
16	43	44.8	494	2	D86493
17	43	44.8	534	2	JC5096
18	42	43.8	421	2	T04798
19	42	43.8	479	2	T23508
20	41.5	43.2	293	2	H46544
21	41	42.7	262	1	D69547
22	41	42.7	416	2	A88109
23	41	42.7	454	2	JC4616
24	41	42.7	470	2	A96286
25	41	42.7	510	2	A92997
26	41	42.7	510	2	AC3352
27	41	42.7	519	2	AS8073
28	41	42.7	677	2	T02951
29	40.5	42.2	809	2	F87458

30	40	41.7	425	2	H70456	modulation competi
31	40	41.7	485	2	T34147	hypothetical prote
32	40	41.7	522	2	B71978	hypothetical prote
33	40	41.7	590	2	A40437	glutamic acid-rich
34	40	41.7	808	2	E64914	dimethylsulfoxide
35	40	41.7	828	2	F96535	hypothetical prote
36	40	41.7	884	2	A31928	glucose transport
37	39.5	41.1	463	1	I40661	mult. protein - Cio
38	39	40.6	227	2	S77870	dnak-type molecula
39	39	40.6	294	2	B86703	tRNA isopentenyltr
40	39	40.6	294	2	G95077	tRNA isopentenyltr
41	39	40.6	311	2	D97945	xylose operon regu
42	39	40.6	315	2	F70203	protein kinase pkn
43	39	40.6	505	1	S77034	guanosine-diphosph
44	39	40.6	518	2	A40732	hypothetical prote
45	39	40.6	530	2	A87518	

ALIGNMENTS

RESULT 1
156242
Lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 156242
R:Maliszewski, C.R.; Delespess, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.
J. Immunol. 153, 3574-3583, 1994
A:Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural
A:Reference number: 156242; MUID:95015846; PMID:7930580
A:Accession: 156242
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-510 <RES>
A:Cross-references: GB:S73813; NID:q765255; PIDN:AAB32152.1; PID:q765256

Query Match 78.1% Score 75; DB 2; Length 510;
Best Local Similarity 73.7% Pred No. 9e-05; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 4;

OY 1 KSDTQETYGALDLGASTQ 19
DB 202 ETNNQETFGALDLGASTQ 220

RESULT 2
S63501
aprase (EC 3.6.1.5) - human (fragments)
N:Alternate names: Arp diposphohydrolase
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S63501
R:Christoforidis, S.; Papamarcaki, T.; Galaris, D.; Kellner, R.; Tsolas, O.
Eur. J. Biochem. 234, 66-74, 1995
A:Title: Purification and properties of human placental Arp diposphohydrolase.
A:Reference number: S63501; MUID:96096723; PMID:8529670
A:Accession: S63501
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-3;4-8;9-13;14-20;21-30;31-44 <CHR>
C:Keywords: hydrolase

Query Match 64.6% Score 62; DB 2; Length 44;
Best Local Similarity 85.7% Pred. No. 0.001;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 ETYGALDLGASTQ 19
DB 28 DLVGALDLGASTQ 41

RESULT 3

T04439

hypothetical protein T18B16.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C:Accession: T04439

R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoyge, W.; Bancroft, I.; Mewes, H.W. submitted to the Protein Sequence Database, April 1998

A:Reference number: 215359

A:Accession: T04439

A:Molecule type: DNA

A:Residues: 1-1052 <BEV>

A:Cross-references: EMBL:AL021687

A:Experimental source: cultivar Columbia; BAC clone T18B16

C:Genetics:

A:Map position: 4

A:Insertions: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3

A:Note: T18B16.150

Query Match

Best Local Similarity 55.2%; Score 53; DB 2; Length 1052;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 TYGALDLCGASTQ 19

Db 685 TFGALDLCGSSLQ 697

RESULT 4

S50463

hypothetical protein YER0056 - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002

C:Accession: S50463

R:Dieckrich, F.S. submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9667, and lambda

A:Reference number: S50433

A:Accession: S50463

A:Molecule type: DNA

A:Residues: 1-630 <DIE>

A:Cross-references: EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005; MTPS:YER0056

C:Genetics:

A:Gene: SGD:YND1; MTPS:YER0056

A:Cross-references: SGD:S0000807

A:Map position: 5R

Query Match

Best Local Similarity 54.2%; Score 52; DB 2; Length 630;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TYGALDLCGASTQ 19

Db 179 TFGMDMGASTQ 191

RESULT 5

T39109

probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T39109

R:Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D. submitted to the EMBL Data Library, October 1999

A:Reference number: 221828

A:Accession: T39109

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-556 <BAR>

A:Cross-references: EMBL:AL121741; PIDN:CA57338.1; GSPDB:GN00006; SPDB:SPAC824.08

A:Experimental source: strain 972h-; cosmid 6824

C:Genetics:

A:Gene: SPDB:SPAC824.08

A:Map position: 1

Query Match

Best Local Similarity 53.1%; Score 51; DB 2; Length 556;

Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 TQETYGALDLCGASTQ 19

Db 276 THSTVAVMDLCGASTQ 291

RESULT 6

T16696

hypothetical protein R07E4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16696

R:Miller, N. submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid R07E4.

A:Reference number: Z18561

A:Accession: T16696

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-557 <MTL>

A:Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AA80403.1; CESP:R0

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:R07E4.4

A:Insertions: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match

Best Local Similarity 52.1%; Score 50; DB 2; Length 557;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETYGALDLCGASTQ 19

Db 212 QKTVGMIDMGASTQ 226

RESULT 7

D86276

hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: D86276

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huizart, L. Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86276

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <STO>

A:Cross-references: GB:AB05172; NID:g5080801; PIDN:AA39311.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match

Best Local Similarity 51.0%; Score 49; DB 2; Length 483;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 SQTQETYGALDLCGASTQ 19

Db 212 TDPLETTGIVELGASQ 229

RESULT 8

FAD02

Profilin II - slime mold (*Dictyostelium discoideum*)C:Species: *Dictyostelium discoideum*

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999

C:Accession: B53255; S18028

R:Haugwitz, M.; Noegel, A.A.; Rieger, D.; Lotspeich, F.; Schleicher, M.

J. Cell Sci. 100, 481-489, 1991

A:Title: *Dictyostelium discoideum* contains two profilin isoforms that differ in structure

A:Reference number: A53255; MUID:92226170; PMID:1725525

A:Accession: B53255

A:Molecule type: mRNA

A:Residues: 1-124 <RH2>

A:Cross-references: EMBL:X61580; NID:q7325; PIDN:CAA3780.1; PID:q7326

A>Note: parts of this sequence, including the amino end of the mature protein, were conf

C:Superfamily: profilin

C:Keywords: actin binding; methylated amino acid

F:2-124/product: profilin II #status experimental <MAT>

F:102/modified site: N6,N6-trimethyllysine (Lys) #status predicted

Query Match 49.0% Score 47; DB 1; Length 124;

Best Local Similarity 60.0% Pred. NO. 1.2;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 1 KSDPTETGALDLCG 15

Db 70 KSDPTATGKLGAGC 84

RESULT 9

T40856

Probable nucleotide phosphatase - fission yeast (*Schizosaccharomyces pombe*)C:Species: *Schizosaccharomyces pombe*

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40856

R:Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21952

A:Accession: T40856

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-572 <RAW>

A:Cross-references: EMBL:AL121783; PIDN:CA857847.1; GSPDB:GN00068; SPDB:SPCC11E10.05C

A:Experimental source: strain 972h-; cosmid c11E10

C:Genetics:

A:Gene: SPDB:SPCC11E10.05C

A:Map position: 3

Query Match 48.4% Score 46.5; DB 2; Length 572;

Best Local Similarity 57.9% Pred. NO. 7.8;

Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Oy 1 KSDPTETGALDLCGASQ 19

Db 162 EKDT-STVGFLDMGASVQ 179

RESULT 10

C70741

Hypothetical protein RV1356 - *Mycobacterium tuberculosis* (strain H37RV)C:Species: *Mycobacterium tuberculosis*

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: C70741

R:COLE, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; MUID:9825987; PMID:9634230

A:Accession: C70741

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-263 <COL>

A:Cross-references: GB:z75555; GB:AL123456; NID:q3261608; PIDN:CAA9989.1; PID:q4190

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV1356

C:Superfamily: *Mycobacterium tuberculosis* hypothetical protein RV1356c

Query Match 45.8% Score 44; DB 2; Length 263;

Best Local Similarity 57.1% Pred. NO. 8.9;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 2 SDPTETGALDLCG 15

Db 84 SDPTLFAALDLCG 97

RESULT 11

S56505

Hypothetical 41.9K protein (leuX-fecE intergenic region) - *Escherichia coli* (strain K

N:Alternate names: hypothetical protein O377

C:Species: *Escherichia coli*

C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002

C:Accession: S56505; B65241

R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.

Nucleic Acids Res. 23, 2105-2119, 1995

A:Title: Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from

A:Reference number: S56314; MUID:95334362; PMID:7610040

A:Accession: S56505

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-377 <BUR>

A:Cross-references: EMBL:U14003; NID:q1263172; PIDN:AAA97176.1; PID:q537121

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.

A:Rose, D.J.; Mau, B.; Shaoh, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: B65241

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-377 <BLAT>

A:Cross-references: GB:AE000498; GB:U00096; NID:q2367368; PIDN:AAC77236.1; PID:q17907

A:Experimental source: strain K-12, substrain M61655

C:Genetics:

A:Gene: yjhc

Query Match 45.8% Score 44; DB 2; Length 377;

Best Local Similarity 60.0% Pred. NO. 13;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KSDPTETGALDLCG 15

Db 255 KIDMPTAGSLRIGG 269

RESULT 12

E86276

Hypothetical protein F14L17.1 - *Arabidopsis thaliana*C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: E86276

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mall, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719; PMID:11130712

```
QY      3 DTQETFGALDLGGASTQ 19
          | : | : ||||| |
Db     131 DPLKTTGIVELGASAQ 147
```

increased ATP phosphatase precursor chromatin-associated - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999
C:Accession: S65147, S48859
R:Hsieh, H.L., Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
[with: (date-modified) 1996-09-29]

A: reference: 1597, modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin
A: reference number: 565141, M01D:96197404, PMID:8616230
A: accession: S65147
A: molecule type: mRNA
A: residues: 1-455 <HS2>
A: cross-references: EMBL:Z32743, NID:9563611, PIDN:CA84655.1, PID:9563612
C: superfamily: nucleoside triphosphatase chromatin-associated
C: keywords: nucleus

	2, Conserved	4, Indels	0, Gaps
QY 6 ETYGALDLCGGSQ 19			
Db 189 KTVGYIDLGGSTQ 202			

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
/Accession: G84442

R. Itoh, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beaulieu, M.L.; Town, C.D.; Fujii, C.Y.;
 Jones, K.O.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umayam, L.; Tallon, L.;
 Neuss, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A1>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A1-Reference number: A84420; MUID:20083487; PMID:10617197
 A1-Accession: G84442

A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: GB:AE002093; NID:g3461821; PIDN:AAC32915.1; GSPDB:ON00139
C:Gene: At2g02970
A:Map position: 2

Query Match	45.8%	Score 44;	DB 2;	Length 516;
Best Local Similarity	52.9%;	Pred. No. 19;		
Matches	9;	Conservative	3;	Mismatches 5;
				Indels 0;
				Gaps 0;

211 DPLKTTGIVELGASAQ 227

nuclear antigen EBNA-3A - human herpesvirus 4
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 21-Jul-2000
C:Accession: S27920; G49253; F49253
R:Sample, J.: Young, L.; Martin, B.; Chantman, T.; Kieff, E.; Rickinson, A.; Kieff, E.
submitted to the EMBL Data Library, July 1990
A:Reference number: S27920

A:Accession: S47920
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-925 <SAMB>
A:Cross-references: EMBL:M34440; NID:G330407; PID:AAA893.1; PID:G330408
R:Polillon, A.; Moss, D.; Stumm, R.; Burrows, S.; Sunbier, A.; Misko, I.; Schmidt, C
Eur. J. Immunol. 22, 183-189, 1992
A:Title: Immunological variation of cytotoxic T cell epitopes in different isolates of Eps
A:Reference number: A49034; MUID:92111623; PMID:1370413
A:Accession: G49253
A:Status: preliminary

A: Residues: 114-332 <AP0>
A: Cross-references: GB:757935; NID:9242901; PIDD:924290090.1; PID:924290020
A: Experimental source: human B-type strain Q1MR-JS86
A: Note: sequence extracted from NCBI backbone (NCBIN:79235, NCBIP:79252)
A: Accession: HA9253

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 314-338 <Ap2>
A:Cross-preferences: GB:579234; NID:g242899; PIDN:AA820989.1; PID:g242900
A:Experimental source: human B-type strain AG6753; human B-type strain IAmR
A:Note: sequence extracted from NCBI backbone (NCBIN:79237, NCBI:79254, NCBIN:79234
C:Genids: 112/3
A:Introps: 112/3
C:Superfamily: human herpesvirus 4 nuclear antigen EBNA-3A

Query Match	45.8%;	Score 44;	DB 2;	Length 925;
Best Local Similarity	69.2%;	Pred. No. 35;		
Matches	9;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;

Search completed: February 11, 2003, 18:40:02
Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:22:16 ; Search time 11 seconds
(without alignments)
71.641 Million cell updates/sec

Title: US-09-781-796b-7

Perfect score: 96
Sequence: 1 KSDPTQETGALDLCGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	95.8	510	1 ENP1_PIG	O9MYU4 sus scrofa
2	92	95.8	513	1 ENP1_BOVIN	O18956 bos taurus
3	75	78.1	510	1 ENP1_HUMAN	P49961 homo sapien
4	75	78.1	510	1 ENP1_MOUSE	P55772 mus musculu
5	66	68.8	511	1 ENP1_RAT	P97687 ratus norv
6	66	67.7	469	1 ENP5_MESAU	O9QYCS mesocricetu
7	64	66.7	427	1 ENP5_MOUSE	O9WU9 mus musculu
8	64	66.7	428	1 ENP5_HUMAN	O75356 homo sapien
9	62	64.6	529	1 ENP1_HUMAN	O93295 gallus gall
10	58	60.4	493	1 ENP1_CHICK	O9Y313 homo sapien
11	56	58.3	495	1 ENP2_HUMAN	O55026 mus musculu
12	56	58.3	495	1 ENP2_MOUSE	O55026 mus musculu
13	56	58.3	495	1 ENP2_RAT	O55026 mus musculu
14	54	56.2	494	1 ENP2_CHICK	P79784 gallus gall
15	52	54.2	630	1 YND1_YEAST	P40009 saccharomyc
16	50	52.1	552	1 YND4_CAEEL	O21815 caenorhabd
17	48	50.0	455	1 ENP6_RAT	O96331 ratus norv
18	48	50.0	455	1 ENP4_MOUSE	O96331 ratus norv
19	47	49.0	124	1 PPO2_DICDI	O96331 ratus norv
20	47	49.0	124	1 ENP4_HUMAN	P26200 dicystosell
21	46	47.9	484	1 ENP6_HUMAN	O75356 homo sapien
22	46	47.9	484	1 RK3_GUTHR	O46894 guillardia
23	44	45.8	263	1 YD56_MYCTU	O11026 mycobacteri
24	44	45.8	372	1 YDHC_ECOLI	P39355 escherichia
25	44	45.8	455	1 NTPA_PEA	P52914 pisum sativ
26	41	42.7	454	1 APY_SOLFU	P80593 solanum tub
27	41	42.7	519	1 ZN3_HUMAN	P13662 homo sapien
28	40	41.7	439	1 PRS4_DROME	P46601 drosophila
29	40	41.7	485	1 YV4E_CAEEL	O18401 caenorhabd
30	40	41.7	808	1 YNFE_ECOLI	P7374 escherichia
31	39	40.6	818	1 SNF3_YEAST	P10870 saccharomyc
32	39	40.6	294	1 MIAA_LACIA	O9CHU2 lactococcus
33	39	40.6	294	1 MIAA_STRPN	O971W3 streptococ

34	39	40.6	505	1 SPKD_STVNY3	P54735 synechocyst
35	39	40.6	518	1 GDA1_YEAST	P32621 saccharomyc
36	39	40.6	591	1 DNAK_MYCCA	P45958 mycoplasma
37	39	40.6	1433	1 Y310_HUMAN	O15027 homo sapien
38	38.5	40.1	299	1 MIAA_STRPY	O96059 streptococ
39	38	39.6	195	1 IRX7_HUMAN	P78412 homo sapien
40	38	39.6	237	1 VDO3_VACCC	P21009 vaccinia vi
41	38	39.6	237	1 VDO3_VACCV	P04302 vaccinia vi
42	38	39.6	227	1 VDO3_VARY	P33068 variola vir
43	38	39.6	332	1 AXHA_ASPRG	P79019 aspergillus
44	38	39.6	509	1 STR_ACTIC	O43990 actinobact
45	38	39.6	587	1 MCCB_ARATH	O91dd8 arabidopsis

ALIGNMENTS

RESULT 1
ENP1_PIG STANDARD: PRT: 510 AA.
AC ENP1_PIG
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-ATPase) (CD39 antigen).
GN ENTP1 OR CD39.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RX MEDLINE=20325090; PubMed=10866813;
RA Lemmens R., Vanduffel L., Kiltel A., Beaudoin A.R., Benrezaak O.,
RT triphosphate diphosphohydrolase-1".
RT Eur. J. Biochem. 267:4106-4114(2000).
RN [2]
RP SEQUENCE OF 202-220.
RC TISSUE=Pancreas;
RX MEDLINE=97115858; PubMed=6955160;
RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RT Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase".
RT J. Biol. Chem. 271:33116-33122(1996).
CC - FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
CC HYDROLYSES ATP AND ADP EQUALLY WELL.
CC - CATALYTIC ACTIVITY: ATP + 2 H(2)O -> AMP + 2 phosphate.
CC - COFACTOR: REDUCES CALCIUM AND MAGNESIUM (BY SIMILARITY).
CC - SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC - TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN VASCULAR
CC ENDOTHELIUM, SMOOTH MUSCLE, SPLEEN AND LUNG.
CC - PTM: CLEAVED IN TWO POLYPEPTIDES THAT SEEM TO STAY TOGETHER BY
CC NONCOVALENT INTERACTIONS.
CC - SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
CC
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CC
CC EMBL, AJ133746; CAB95871.1; -

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CC -----
DR EMBL; AF005940; AAB62382.1; -
DR InterPro; IPR000407; GDAL-CD39_NTPase.
DR Pfam; PF01150; GDAL-CD39-1.
DR PROSITE; PS01238; GDAL-CD39_NTPASE; 1.
KM Hydrolyase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 481
FT TRANSMEM 482 502
FT DOMAIN 503 513
FT CAROAHND 73 73
FT CAROAHND 227 227
FT CAROAHND 245 245
FT CAROAHND 307 307
FT CAROAHND 336 336
FT CAROAHND 373 373
FT CAROAHND 460 460
FT CONFLICT 97 97
FT CONFLICT 101 103
FT CONFLICT 464 464
SQ SEQUENCE 513 AA; 58113 MW; 20FED8F27B6D2P96 CRC64;
Query Match 95.8%; Score 92; DB 1; Length 513;
Best Local Similarity 94.7%; Pred. No. 2,5e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSDTQETFGALDGGASTQ 19
DB 202 KDDTQETFGALDGGASTQ 220
I|||||I|||||I|||||I
ENP1_HUMAN STANDARD: PRT; 510 AA.
ID ENP1_HUMAN
AC P49961; Q9U0Q9; Q9Y3Q9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN ENTPD1 OR CD39.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
[1]
SEQUENCE FROM N.A. (ISOFORM VASCULAR).
RA MEDLINE-95015846; PubMed-7930580;
RA Malszewski C.R., Delespese G.U.T., Schoenborn M.A., Armistage R.J.,
RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poul Dexter K.,
RA Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;
RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
RT structural characterization."
RT J. Immunol. 153:3574-3583(1994).
[2]
SEQUENCE FROM N.A. (ISOFORM VASCULAR).
RA MEDLINE-97149443; PubMed-8996251;
RA Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Kozlak K.,
RA Millan M., Hancock W.W., Bach F.H.;
RT "Loss of ATP diphosphohydrolase activity with endothelial cell
RT activation."
RT J. Exp. Med. 185:153-163(1997).

```

[3] SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND II).
 RC TISSUE=Placenta; PubMed=10405171;
 RX MEDLINE=9933082; PubMed=10405171;
 RA Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,
 RT Titani K., Fujimura Y., Narita N.;
 RL "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
 and II.";
 RN FEBS Lett. 453:335-340(1999).
 [4]
 RP SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.
 RC TISSUE=Placenta;
 RX MEDLINE=96096722; PubMed=8529670;
 RA Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;
 RT "Purification and properties of human placental ATP
 diphosphohydrolase.";
 RL Eur. J. Biochem. 234:66-74(1995).
 [5]
 RP SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND
 RP 399-405 (ISOFORM PLACENTAL I).
 RC TISSUE=Placenta;
 RX MEDLINE=9906244; PubMed=9846014;
 RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
 RT Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.;
 RL "Placental ecto-ATP diphosphohydrolase: Its structural feature
 distinct from CD39, localization and inhibition on shear-induced
 platelet aggregation.";
 RL Int. J. Hematol. 68:297-310(1998).
 [6]
 RP FUNCTION.
 RP MEDLINE=97115858; PubMed=8955160;
 RA Kaczmarek E., Kozlak K., Sevigny J., Stegel J.B., Anrather J.,
 RL Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 [7]
 RL FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
 NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
 BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
 CC HYDROLYSES ATP AND ADP EQUALLY WELL.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBUNIT: HOMODIMER: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: 3 ISOFORMS: VASCULAR (SHOWN HERE), PLACENTAL
 CC I AND PLACENTAL II; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY ON ACTIVATED LYMPHOID
 CC CELLS. ALSO EXPRESSED IN ENDOTHELIAL TISSUES. THE VASCULAR ISOFORM
 CC AND THE PLACENTAL ISOFORM II ARE PRESENT IN BOTH PLACENTA AND
 CC UMBILICAL VEIN, WHEREAS PLACENTAL ISOFORM I IS PRESENT IN PLACENTA
 CC ONLY.
 CC -1- PTH: THE N-TERMINUS IS BLOCKED.
 CC -1- MISCELLANEOUS: OPTIMAL PH IS 7.0-7.5 WITH ATP AS SUBSTRATE AND
 CC 7.5-8.0 WITH ADP.
 CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd39.htm".
 CC
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 CC
 CC EMBL: S73813; AAB32152.1; -;
 CC EMBL: U87967; AAB47572.1; -;
 CC EMBL: AJ133133; CAB41866.1; -;
 CC EMBL: AJ133134; CAB41867.1; -;
 CC Genbank: HGNC:3363; ENTPD1.
 CC MIM: 601752; -;
 CC InterPro: IPR000407; GDAL_CD39_NTPase.

DR Pfam: PF01150; GDAL_CD39; 1.
 DR PROSITE: PS01238; GDAL_CD39_NTPASE; 1.
 KW Hydrolyase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium;
 KW Alternative splicing.
 FT DOMAIN 1 16
 FT TRANSMEM 17 37
 FT TRANSMEM 38 476
 FT TRANSMEM 479 499
 FT DOMAIN 500 510
 FT CARBOHYD 73 73
 FT CARBOHYD 227 227
 FT CARBOHYD 292 292
 FT CARBOHYD 334 334
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 FT CARBOHYD 457 457
 FT VARSPPLIC 1 4
 FT VARSPPLIC 272 299
 FT VARSPPLIC 300 510
 FT CONFLICT 57 58
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 SQ SEQUENCE 510 AA; 57964 MW; BAD87D2499649159 CRC64;
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 Best Local Similarity 73.7%; Pred. No. 2.3e-05;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KSDPTETGALDUGASTQ 19
 DB 202 ETNNQETFPALDUGASTQ 220
 ID ENTPD_MOUSE STRAND: PRT; 510 AA.
 AC P55772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ecconocleotide triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (lymphoid cell
 DE activation antigen) (Ecto-ATPase) (CD39 antigen).
 GN ENTPD1 OR CD39.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=95015846; PubMed=7930580;
 RA Maliszewski C.R., Delespessis G.J.T., Schoenborn M.A., Armitage R.J.,
 RA Fawcett W.C., Nakajima T., Baker E., Sutherland G.R., Polinder K.,
 RA Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
 RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
 RT structural characterization.";
 RL J. Immunol. 153:3574-3583(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98399871; PubMed=9730622;
 RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
 RA Gayle R.B. III, Maliszewski C.R.;
 RT "Gene structure and chromosome location of mouse CD39 coding for an
 RT ecto-ATPase.";
 RL Cytogenet. Cell Genet. 81:287-289(1998).
 CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
 CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
 CC HYDROLYSES ATP AND ADP EQUALLY WELL.

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RP SEQUENCE FROM N.A.
RC STRAIN-Wistar. TISSUE-Cochlea;
RX MEDLINE=20050856; PubMed=10581401;
RA Vlahovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
RT Evidence for alternative splicing of ecto-ATPase associated with
RT termination of purinergic transmission."
RN Brain Res. Mol. Brain Res. 73:85-92(1999).
RP
RC SEQUENCE OF 432-511 FROM N.A.
RC STRAIN-Sprague-Dawley. TISSUE-Brain;
RX MEDLINE=98031057; PubMed=9364474;
RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
RT rat brain."
RL Neuropharmacology 36:1189-1200(1997).
CC
CC -I- FUNCTION. IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
CC HYDROLYSES ATP AND ADP EQUALLY WELL.
CC -I- CATALYTIC ACTIVITY: ATP + 2 H2O = AMP + 2 phosphate.
CC -I- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
CC -I- SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: EXPRESSED IN PRIMARY NEURONS AND ASTROCYTES,
CC KIDNEY, LIVER, MUSCLE, THYMUS, LUNG AND SPLEEN.
CC -I- PTM: N-GLYCOSYLATED.
CC -I- SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.
CC -----
CC
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CC -----
DR EMBL: U81295; AAC53195.1; -
DR EMBL: Y15685; CAN75730.1; -
DR InterPro: IPR000407; GDAI_CD39_NTPase.
DR Pfam: PF01150; GDAI_CD39; 1.
DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolyase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT DOMAIN 1 17 37
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CC Ectonucleoside triphosphate diphosphohydrolase 5 precursor
 CC (EC 3.6.1.6) (NTPase5) (Nucleoside diphosphatase) (CD39 antigen-like
 DE 4) (ER-UDPase) (Proto-oncogene cph).
 GN ENTPD5 OR CD39L4 OR CPH.
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 CC NCBI_TaxID=10036;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99142925; PubMed=9989819;
 RA Velasco J.A., Avila M.A., Notario V.;
 RT "The product of the cph oncogene is a truncated, nucleotide-binding
 RT protein that enhances cellular survival to stress";
 RL Oncogene 18:689-701(1999).
 CC -1- FUNCTION: LIKELY TO PROMOTE REGIOCYTATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES. NOR THIAMINE PYRROPHOSPHATE
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 CC nucleotide + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL CELLS AND MOST ADULT
 CC TISSUES.
 CC -1- DISEASE: CPH ONCOGENE HAS TRANSFORMING CAPACITY AND TUMORIGENIC
 CC POTENTIAL.
 CC -1- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
 CC -----
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 CC DR EMBL: AF084569; AAF22932.1; -
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 CC DR Pfam: PF01150; GDA1_CD39; 1.
 CC DR PROSITE: PS01238; GDA1_CD39_NTPase; FALSE_NEG.
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 CC ENTP5_MOUSE STANDARD; PRT; 427 AA.
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 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
 CC (EC 3.6.1.6) (NTPase5) (Nucleoside diphosphatase) (CD39 antigen-like
 CC 4) (ER-UDPase).
 CC GN ENTPD5 OR CD39L4.

OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 CC TISSUE-Testis;
 RX MEDLINE=98119025; PubMed=9457681;
 RA Chadwick B.P., Williamson J., Sheer D., Frischaut A.-M.;
 RT "cDNA cloning and chromosomal mapping of a mouse gene with homology to
 RT NTPases";
 RL Mamm. Genome 9:162-164(1998).
 RN [2]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION.
 CC TISSUE-Liver;
 RX MEDLINE=99298181; PubMed=10369669;
 RA Trombetta E.S., Helentius A.;
 RT "Glycoprotein reglucosylation and nucleotide sugar utilization in the
 RT secretory pathway: identification of a nucleoside diphosphatase in the
 RT endoplasmic reticulum";
 RL EMBO J. 18:3282-3292(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21083660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kesukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Leischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Carlini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Notodane P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: LIKELY TO PROMOTE REGIOCYTATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES. NOR THIAMINE
 CC PYRROPHOSPHATE.
 CC -1- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 CC nucleotide + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- PTM: GLYCOSYLATED WITH HIGH MANNOSE N-LINKED GLYCANS.
 CC -1- MISCELLANEOUS: OPTIMAL PH IS NEUTRAL.
 CC -1- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: AF006482; AAC05181.1; -
 CC DR EMBL: AJ238636; CAB45533.1; -
 CC DR EMBL: AK002618; BAB22234.1; -
 CC DR MGD: MGI:1321385; Entpd5
 CC InterPro: IPR000407; GDA1_CD39_NTPase.
 CC DR Pfam: PF01150; GDA1_CD39; 1.

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DR PROSITE: PS01238: G0AL_CD39_NTPASE: FALSE NEG.
KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal.
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Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps

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Db 192 QETVETLDGGASTQ 206
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RESULT 9
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AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ectonucleoside triphosphate diphosphohydrolase 3 (EC 3.6.1.5)
DE (NPfases3) (Ecto-ATP diphosphohydrolase) (ATPase) (Ecto-apyrase)
DE (CD39 antigen-like 3) (HB6).
GN ENTPD3 OR CD39L3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Keratinocytes;
RX MEDLINE=98341119; PubMed=9676430;
RA Chadwick B.P., Frischman A.-M.;
RT "The CD39-like gene family: identification of three new human members
RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
RT the gene family from Drosophila melanogaster.";
RL Genomics 50:357-367(1998).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP TISSUE=Brain;
RX MEDLINE=98342144; PubMed=9675246;
RA Smith T.M., Kirley T.L.;
RT "Cloning, sequencing, and expression of a human brain ecto-apyrase
RT related to both the ecto-NTPases and CD39 ecto-apyrases.";
RL Biochim. Biophys. Acta 1386:65-78(1998).
RN [3]
RP REVISIONS.
RP Smith T.M., Kirley T.L.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP MUTAGENESIS OF TRP-187; ASP-219 AND TRP-459.
RX MEDLINE=99249795; PubMed=1023136;
RA Smith T.M., Lewis Carl S.A., Smith T.M., Kirley T.L.;
RT "Mutagenesis of two conserved tryptophan residues of the E-type
RT ATPases: inactivation and conversion of an ecto-apyrase to an
RT ecto-NTPase.";
RL Biochemistry 38:5849-5857(1999).
RN [5]
RP MUTAGENESIS OF R-67; R-143; R-146; E-182; N-191; S-224 AND Q-226.
RX MEDLINE=21197753; PubMed=11300744;
RA Yang F., Hicks-Berger C.A., Smith T.M., Kirley T.L.;
RT Site-directed mutagenesis of human nucleoside triphosphate
RT diphosphohydrolase 3: the importance of residues in the apyrase
RT conserved regions.";
RL Biochemistry 40:3943-3950(2001).

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Query Match	Best Local Similarity	Score 56;	DB 1;	Length 495;	
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RESULT 12					
ENP2.MOUSE					
ID ENP2.MOUSE	STANDARD:	PRT:	495 AA.		
AC 055026:	035928;	09DCR9;			
DT 16-OCT-2001 (Rel. 40, Created)					
DT 16-OCT-2001 (Rel. 40, Last sequence update)					
DE Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)					
DE (NTPDase2) (ecto-ATPase) (CD39 antigen-like 1).					
GN ENP2D OR CD91L.					
OS Mus musculus (Mouse).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX NCBI_TaxID=10090;					
RN [1]					
RP SEQUENCE FROM N.A. (SHORT FORM).					
RC TISSUE=Embryo;					
RC MEDLINE=97419269; PubMed=9271669;					
RA Chadwick B.P., Erischauf A.-M.,					
RT "Cloning and mapping of a human and mouse gene with homology to ecto-					
RT ATPase genes.";					
RT Mamm. Genome 8: 668-672(1997).					
RN [2]					
RP SEQUENCE FROM N.A. (LONG FORM).					
RC TISSUE=Hepatoima;					
RC MEDLINE=98288263; PubMed=9624117;					
RA Gao L., Dong L., Whitlock J.P., Jr.;					
RT "A novel response to dioxin. Induction of ecto-ATPase gene					
RT expression.";					
RT J. Biol. Chem. 273:15358-15365(1998).					
RN [3]					
RP SEQUENCE FROM N.A. (LONG FORM).					
RC STRAIN=C57BL/6J; TISSUE=Kidney;					
RA MEDLINE=21085660; PubMed=11217851;					
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,					
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,					
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,					
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,					
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,					
RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,					
RA Schirral L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Mashio T.,					
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barz G.,					
RA Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,					
RA Brownstein M.T., Bult C., Fletcher C., Fujita M., Gonzalez M.,					
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,					
RA Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P.,					
RA Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,					
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,					
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,					
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,					
RA Hayashizaki Y.;					
RT "Functional annotation of a full-length mouse cDNA collection.";					
RT Mamm. Genome 409:685-690(2001).					
CC -!- FUNCTION: TO REGULATE PURINE/PIRIMIDINE METABOLISM AND OTHER					
NUCLEOTIDES TO THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER					

CC ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- INDUCTION: BY DIOXIN.
 CC -1- PIM: HAS PROBABLY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U91511; AAB81014.1; -
 CC EMBL: AF042811; AAC24347.1; -
 CC EMBL: AK002553; BAB22182.1; -
 CC MGD: MGI:1096863; Entp2.
 CC InterPro: IPR000407; GDAL_CD39_NTPase.
 CC Pfam: PF01150; GDAL_CD39_1.
 CC DR PROSITE: PS01238; GDAL_CD39_NTPase; 1.
 CC KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 CC Alternative splicing.
 CC FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 5 25 POTENTIAL.
 CC FT DOMAIN 26 462 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 463 483 POTENTIAL.
 CC FT DOMAIN 484 495 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPPLIC 130 132 LTS -> MAG (IN SHORT ISOFORM).
 CC FT VARSPPLIC 133 495 MISSING (IN SHORT ISOFORM).
 CC FT CONFLICT 400 400 T -> A (IN REF. 3).
 CC FT CONFLICT 414 414 S -> R (IN REF. 3).
 CC FT CONFLICT 437 437 T -> A (IN REF. 3).
 CC SQ SEQUENCE 495 AA; 54310 MW; CC081IC5D79CACC8 CRC64;
 CC -----
 CC Query Match 58.38; Score 56; DB 1; Length 495;
 CC Best Local Similarity 84.68; Pred. No. 0.046; 1; Indels 0; Gaps 0;
 CC Matches 11; Conservative 1; Mismatches 1;
 CC -----
 CC OY 7 TYGALDILGASTQ 19
 CC DB 196 TLGAMDLGASTQ 208
 CC -----
 CC RESULT 13
 CC ENP2_RAT STANDARD: PRT; 495 AA.
 CC AC 035795; 09JHY5; 09WVET;
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
 CC DE (NTPase2) (Ecto-ATPase) (CD39 antigen-like 1).
 CC GN ENTPD2 OR CD39L1.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OK MBLTAXID=01116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 CC RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 CC RX MEDLINE=98031057; PubMed=9364474;
 CC RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;

RT "an ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
 RT rat brain.";
 RT RL Neuropharmacology 36:1189-1200(1997).
 RN [2]
 RN RP SEQUENCE FROM N.A. (ISOFORM 1).
 RN RC STRAIN=Sprague-Dawley; TISSUE=Sertoli cells;
 RN RX MEDLINE=21121474; PubMed=11229804;
 RN RT Lu Q., Porter L.D., Cui X., Sanborn B.M.;
 RN J. Androl. 22:289-301(2001).
 RN [3]
 RN RP SEQUENCE OF 379-495 FROM N.A. (ISOFORM 2).
 RN RC STRAIN=Wistar; TISSUE=Cochlea;
 RN RX MEDLINE=20050856; PubMed=10581401;
 RN RA Vlakovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
 RN RT "Evidence for alternative splicing of ecto-ATPase associated with
 RN termination of purinergic transmission.";
 RN Brain Res. Mol. Brain Res. 73:85-92(1999).
 CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES
 CC ADP ONLY TO A MARGINAL EXTENT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, VAS DEFERENS,
 CC KIDNEY, SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION
 CC IN LIVER.
 CC -1- INDUCTION: BY FSH IN SERTOLI CELLS BUT NOT IN PERTUBULAR CELLS;
 CC BY CAMP IN BOTH TYPE OF CELLS.
 CC -1- PIM: HAS PROBABLY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y11835; CAAT2533.1; -
 CC EMBL: AF276940; AAF87740.1; -
 CC EMBL: AF129103; AAD2303.1; -
 CC InterPro: IPR000407; GDAL_CD39_NTPase.
 CC DR Pfam: PF01150; GDAL_CD39_1.
 CC DR PROSITE: PS01238; GDAL_CD39_NTPase; 1.
 CC KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 CC Alternative splicing.
 CC FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 5 25 POTENTIAL.
 CC FT DOMAIN 26 462 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 463 483 POTENTIAL.
 CC FT DOMAIN 484 495 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPPLIC 486 495 VRSKSPGAL -> DVRSQPVTOGEVHSMDRCSDLOGPGR
 CC FLGSPLEAPPEPCWESVPCLLVTKFVAKDES (IN
 CC ISOFORM 2).
 CC FT CONFLICT 20 20 T -> A (IN REF. 2).
 CC FT CONFLICT 127 128 PF -> LF (IN REF. 2).
 CC FT CONFLICT 339 339 A -> T (IN REF. 2).
 CC FT CONFLICT 444 444 L -> F (IN REF. 2).
 CC SQ SEQUENCE 495 AA; 54389 MW; 237B999F1BBB8E00 CRC64;
 CC -----
 CC Query Match 58.38; Score 56; DB 1; Length 495;
 CC Best Local Similarity 84.68; Pred. No. 0.046;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 7 TYGALDLCGASTQ 19
 Db 196 TLGAMDLCGASTQ 208

RESULT 14

ENP2_CHICK
 AC P79784; STANDARD; PRT: 494 AA.

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ectonucleoside triphosphate dihydrolyase 2 (EC 3.6.1.3)
 DE (NTPase2) (ecto-ATPase) (CD39 antigen like 1).
 DE ENPMP2 OR CD39L1.

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 68-73; 83-90; 108; 121;
 RP 144-150; 154-176; 208-217; 251-258; 273-284; 337-352; 374-380;
 RP 383-389; 448-456 AND 459-479.
 RC TISSUE=Skkeletal muscle, and Glizzard;
 RX MEDLINE=97150869; PubMed=8995405;

RA Kirley T.L.;
 RT "Complementary DNA cloning and sequencing of the chicken muscle ecto-
 RT ATPase. Homology with the lymphoid cell activation antigen CD39.";
 RT J. Biol. Chem. 272:1076-1081(1997).

RP SEQUENCE OF 1-12 AND 154-176, AND CHARACTERIZATION.
 RX MEDLINE=95081479; PubMed=7989647;

RA Stout J.G., Kirley T.L.;

RT "Purification and characterization of the ecto-mg-ATPase of chicken
 RT glizzard smooth muscle.";

RA J. Biochem. Biophys. Methods 29:61-75(1994).

CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYZE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES
 CC ADP ONLY TO A MAGNICAL EXTENT (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.

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DR EMBL: U74467; AAC60071.1; -;
 DR InterPro: IPR000407; GDAL_CD39_NTPase.

DR Pfam: PF01150; GDAL_CD39.1.

DR PROSITE: PS01238; GDAL_CD39_NTPASE.1.

KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium.

FT INTL MET 0

FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 4 24 POTENTIAL.

FT DOMAIN 25 464 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 465 485 POTENTIAL.

FT DOMAIN 486 494 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 8 13 POLY-LEU.

FT CARBOHYD 61 61 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT CARBOHYD 417 417 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT CARBOHYD 443 443 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT CONFLICT 11 11 L -> LL (IN REF. 2).

FT CONFLICT 174 176 ENF -> GNM (IN REF. 2).
 ..SQ SEQUENCE 494 AA; 54402 MW; 1E0E0651DA621EE CRC64;

Query Match
 best Local Similarity 66.7%; Score 54; DB 1; Length 494;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 OERTYALDLCGASTQ 19
 Db 190 KTLGAMDLCGASTQ 204

RESULT 15

YNDL_YEAST
 AC P40009; STANDARD; PRT: 630 AA.

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Golgi apyrase (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine
 DE diphosphatase) (ADPase) (ATP-diphosphohydrolase) (Golgi nucleoside
 DE diphosphatase).

DE YNDL OR YER005W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

ON NCBI_TaxID=4932;

ON [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,

RA Aviles E., Berro A., Brennan T., Carpenter J., Chen E., Cherry J.M.,

RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,

RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,

RA Moselele D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,

RA Petzel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,

RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;

RA Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC STRAIN=S288C.

RX MEDLINE=99340091; PubMed=10409709;

RA Gao X.D., Kaligorov V., Jigami Y.;

RT "YNDL, a homologue of GDAL, encodes membrane-bound apyrase required
 RT for Golgi N- and O-glycosylation in Saccharomyces cerevisiae.";

RL J. Biol. Chem. 274:21450-21456(1999)

CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF PHOSPHANHYDRIDE BONDS OF
 CC NUCLEOSIDE TRI- AND DI-PHOSPHATES. HAS EQUAL HIGH ACTIVITY TOWARD
 CC ADP/ATP, GDP/GTP, AND UDP/UTP AND APPROXIMATELY 50% LESS TOWARD
 CC CDP/CTP AND THIMINE PYROPHOSPHATE. HAS NO ACTIVITY TOWARD GMP.

CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.

CC -1- PATHWAY: Glycosylation.

CC -1- SUBCELLULAR LOCATION: MEMBRANE BOUND; GOLGI.

CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.

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DR EMBL: U18778; AAB64538.1; -;

DR EMBL: AF203695; AAF17573.1; -;

DR SGD: S0000807; YNDL.

DR InterPro: IPR000407; GDAL_CD39_NTPase.

DR Pfam: PF01150; GDAL_CD39.1.

DR PROSITE: PS01238; GDAL_CD39_NTPASE.1.

KW Hydrolyase; Transmembrane; Golgi stack.

FT DOMAIN 1 500 LUMENAL (POTENTIAL).

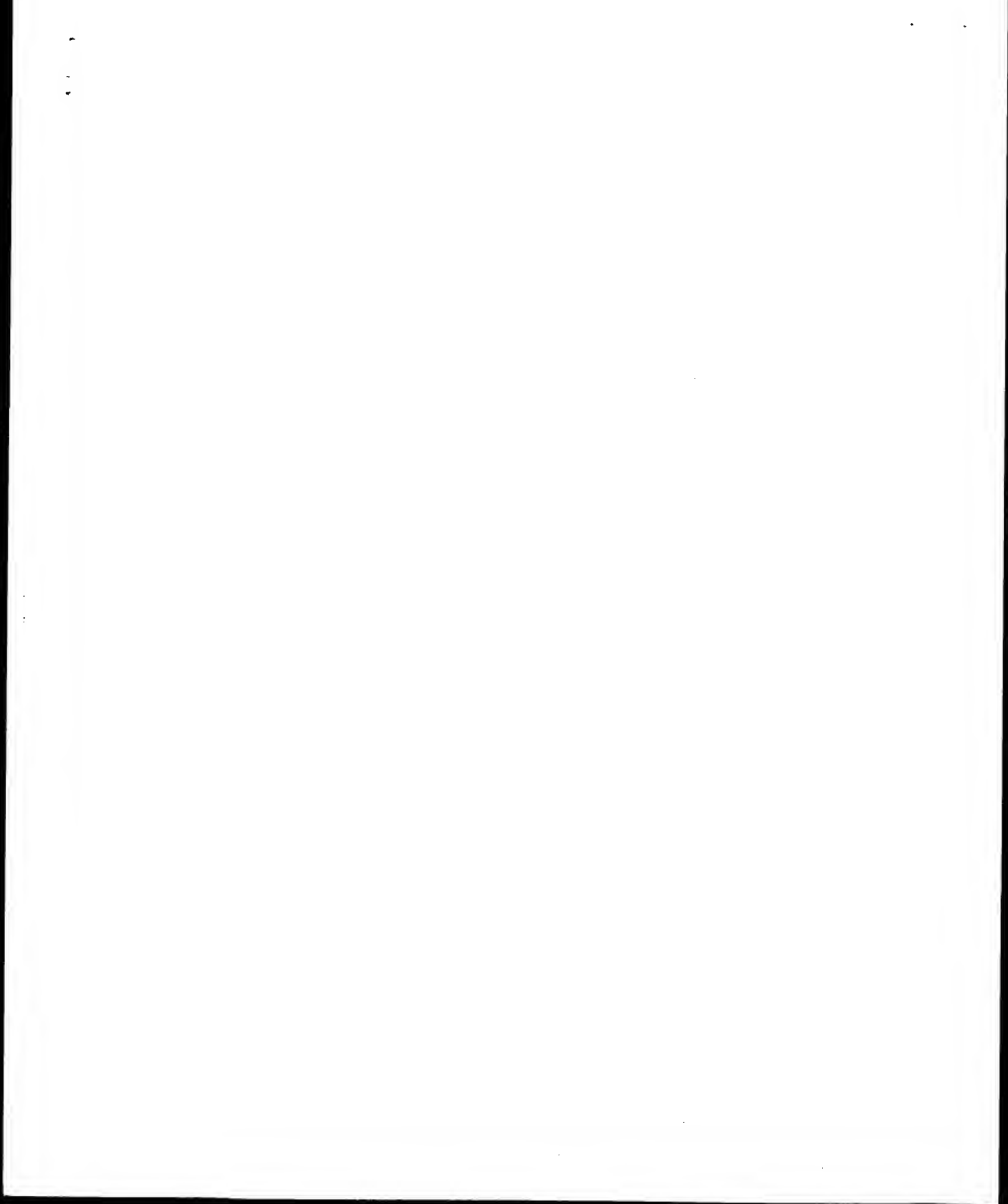
FT TRANSMEM 501 517 POTENTIAL.

FT DOMAIN 518 630 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 630 AA: 71851 MW: 02F8D24A78212544 CRC64;

Query Match 54.2%; Score 52; DB 1; Length 630;
Best Local Similarity 69.2%; Pred. No. 0.3;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TFGALDLGGASTQ 19
1:1:1:1:1:1:1
Db 179 TFGFMDMGASTQ 191

Search completed: February 11, 2003, 18:38:00
Job time : 12 secs



GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: February 11, 2003, 18:33:31 ; Search time 92 Seconds
(without alignments)
42.553 Million cell updates/sec

Title: US-09-781-796b-7

Sequence: 1 KSDPTQFYGALDLCGASTQ 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriophage:*
17: sp.archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	78.1	510	11	Q92106
2	64	66.7	407	4	Q8WUB3
3	64	66.7	428	4	Q96RX0
4	58	60.4	493	13	Q90X66
5	58	60.4	681	10	Q86613
6	56	58.3	495	11	Q921R1
7	54	56.2	300	11	Q90813
8	53	55.2	1052	10	Q49676
9	51	53.1	556	3	Q9UT35
10	49	51.0	483	10	Q9X162
11	48	50.0	447	10	Q9FU11
12	48	50.0	448	11	Q8R0U1
13	48	50.0	462	10	Q9YEC9
14	48	50.0	635	10	Q857F1
15	47	49.0	467	10	Q8RV76
16	47	49.0	606	11	Q9ET10

17	47	49.0	690	5	Q9BHV5	Q9bhv5 leishmania
18	46.5	48.4	572	3	Q9USP2	Q9usp2 schizosacch
19	46.5	48.4	604	4	Q9NOZ7	Q9ngz7 homo sapien
20	46	47.9	148	10	Q9XGR6	Q9xgr6 xanthoceras
21	46	47.9	483	4	Q8TAS7	Q8tas7 homo sapien
22	46	47.9	550	4	Q9NTN2	Q9ntn2 homo sapien
23	45	46.9	476	2	Q9RO11	Q9rq11 bacteroides
24	44.5	46.4	326	10	Q9AUI4	Q9aul4 medicago tr
25	44	45.8	405	10	Q9M9T7	Q9m9t7 arabidopsis
26	44	45.8	407	10	Q9AVN8	Q9avn8 pisum sativ
27	44	45.8	447	10	Q9SLV4	Q9slv4 pisum sativ
28	44	45.8	455	10	Q9FEA6	Q9fea6 pisum sativ
29	44	45.8	455	10	Q8RVU0	Q8rvu0 pisum sativ
30	44	45.8	455	10	Q8RWT9	Q8rwt9 pisum sativ
31	44	45.8	461	5	Q76268	Q76268 diosiphila
32	44	45.8	464	5	Q9V018	Q9v018 diosiphila
33	44	45.8	471	10	Q9SOG2	Q9sog2 arabidopsis
34	44	45.8	472	10	Q9M7B3	Q9m7b3 arabidopsis
35	44	45.8	472	10	Q9SPW5	Q9spw5 arabidopsis
36	44	45.8	473	10	Q8RWT8	Q8rwt8 pisum sativ
37	44	45.8	555	10	Q8AEZ2	Q8aez2 arabidopsis
38	44	45.8	555	10	Q80612	Q80612 arabidopsis
39	44	45.8	925	12	Q69138	Q69138 human hepe
40	44	45.8	2139	3	Q9P880	Q9p880 botrytis cl
41	44	45.8	2225	5	Q9VJ82	Q9vj82 diosiphila
42	43	44.8	313	16	Q9F206	Q9f206 streptomyce
43	43	44.8	456	10	Q9SPW8	Q9spw8 lotus japon
44	43	44.8	468	10	Q9FVC2	Q9fvc2 glycine soj
45	43	44.8	494	16	Q9RB68	Q9rb68 chlamydia p

ALIGNMENTS

RESULT 1
ID Q92106 PRELIMINARY; PRT; 510 AA.

AC Q92106; 01-DEC-2001 (TREMBLrel. 19, created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Similar to ectonucleoside triphosphate dihydrolyase 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011278; AAH11278.1; -
DR InterPro: IPR00407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
DR PROSITE: PS01238; GDA1_CD39_NTPASE; UNKNOWN_1.
KW Hydrolase.
SO SEQUENCE. 510 AA; 57176 MW; E77BB64AE1A13A0 CRC64;

Query Match 78.1%; Score 75; DB 11; Length 510;
Best local Similarity 83.3%; Pred. No. 0.00028;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SDRQETFGALDLCGASTQ 19
DB 202 SDRQETFGALDLCGASTQ 219

RESULT 2

ID Q8WUB3 PRELIMINARY; PRT; 407 AA.
AC Q8WUB3; 01-MAR-2002 (TREMBLrel. 20, created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

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DE Similar to ectonucleoside triphosphate diphosphohydrolase 5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RU Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020966; AAH20966.1;
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
KW Hydrolase.
SQ SEQUENCE 407 AA; 4536 MW; D92AF7DC9CE9E5B CRC64;

Query Match
Best Local Similarity 86.7%; Score 64; DB 4; Length 407;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 OETYGALDGGASTQ 19
DB 192 OETVGTLDGGASTQ 206

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RESULT 3
O96RX0 PRELIMINARY; PRT; 428 AA.
AC O96RX0;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE PcpH proto-oncogene protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20173601; PubMed=10708485;
RA Recto J.A., Zambrano N., Pena, Ld, Reig J.A., Rhoads A., Rouzaut A.,
RA Notario V.;
RT "The human PcpH proto-oncogene: cDNA identification, primary
RT structure, chromosomal mapping, and expression in normal and tumor
RT cells.";
RL Mol. Carcinog. 27:229-236(2000).
DR EMBL; AF136572; AAK82950.1;
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
SQ SEQUENCE 428 AA; 47431 MW; F2C4F7DE650A44F6 CRC64;

Query Match
Best Local Similarity 86.7%; Score 64; DB 4; Length 428;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 OETYGALDGGASTQ 19
DB 192 OETVGTLDGGASTQ 206

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RESULT 4
O90X66 PRELIMINARY; PRT; 493 AA.
AC O90X66;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
RT "Purification, molecular cloning, and expression of the chicken liver
RT ecto-ATP-diphosphohydrolase.";
RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF426405; AAL25086.1;
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 493 AA; 54063 MW; 0380449E86167B70 CRC64;

Query Match
Best Local Similarity 85.7%; Score 58; DB 13; Length 493;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 ETYGALDGGASTQ 19
DB 197 EYLGALDGGASTQ 210

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RESULT 5
O8S613 PRELIMINARY; PRT; 681 AA.
AC O8S613;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Putative nucleoside phosphatase.
GN OSJNB0023M1.10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriaristaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPONBARE;
RA McCombe W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff R.,
RA Kull R., Nascimento L., Baker J., Santos L., Zutavern T., Miller B.,
RA Cummins D.M., Katzenberger F., Miller S., Bell M., Balija V., Shah R.,
RA King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OSJNB0023M1, from chromosome 10, complete sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092749; AAM08556.1;
SQ SEQUENCE 681 AA; 75002 MW; B1E87479202580BD CRC64;

Query Match
Best Local Similarity 61.1%; Score 58; DB 10; Length 681;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SDTETYGALDGGASTQ 19
DB 260 SSSKRYGSLDGGASTQ 277

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RESULT 6
O921R1 PRELIMINARY; PRT; 495 AA.
AC O921R1;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 2.
GN ENRPP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011241; AAH11241.1; -
 DR MGD: MGI:1096863; Etlp42.
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39; 1.
 DR PROSITE: PS01238; GDA1_CD39_NTPase; UNKNOWN_1.
 DR Hydrolyase.
 KW SEQUENCE 495 AA; 54319 MW; A76468A0CBF86AAC CRC64;

Query Match 58.3%; Score 56; DB 11; Length 495;
 Best Local Similarity 84.6%; Pred. No. 0.49;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 TYGALDLAGASTQ 19
 DB 196 TLGAMDLGASTQ 208

RESULT 7
 Q9DB13 PRELIMINARY; PRT; 300 AA.
 AC Q9DB13;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 2010320H07RLK protein.
 GN 2010320H07RLK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinaigawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izaava M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbush J.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakai R., Tomita M., Wagner L., Washio T.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK008590; BAB25764.1; -
 DR MGD: MGI:1919340; 2010320H07RLK.
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39; 1.
 DR SEQUENCE 300 AA; 33646 MW; CCDE372AF12C6B16 CRC64;

Query Match 56.2%; Score 54; DB 11; Length 300;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GADLDGASTQ 19
 DB 4 GADLDGASTQ 14

RESULT 8

O49676 PRELIMINARY; PRT; 1052 AA.
 AC O49676;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Hypothetical 116.4 kDa protein.
 GN T18B16.150 OR AT4G19180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benay M., Benes V., Rechmann S., Borkova D., Ansoorge W., Bancroft I.,
 RA Mewes H.W., Mayer K., Scheller C.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL021687; CA16707.1; -
 DR EMBL: AL161550; CAB78920.1; -
 DR InterPro: IPR000620; DUF6.
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF00892; DUF6; 1.
 DR Pfam: PF01150; GDA1_CD39; 1.
 DR Hypothetical protein.
 KW SEQUENCE 1052 AA; 116388 MW; 88C4AF1F16225987 CRC64;

Query Match 55.2%; Score 53; DB 10; Length 1052;
 Best Local Similarity 76.9%; Pred. No. 3.9;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 TYGALDLAGASTQ 19
 DB 685 TLGALDLAGASTQ 697

RESULT 9
 Q9UT35 PRELIMINARY; PRT; 556 AA.
 AC Q9UT35;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative guanosine-diphosphatase (Guanosine diphosphatase).
 GN SPAC824.08 OR GDP1.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 ON NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Barrell B.G., Rajandream M.A., Quail M., Seagar K., Harris D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanchez R., Franco A., Notario V., Gacto M., Cansado J.;
 RT "Characterization of a guanosine diphosphatase gene from
 Schizosaccharomyces pombe.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL121741; CAB57338.1; -
 DR EMBL: AF465240; AAL69974.1; -
 DR InterPro: IPR000407; GDA1_CD39_NTPase.

DR Pfam: PF01150; GDAI_CD39; 1.
 DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
 SO SEQUENCE 556 AA; 61588 MW; 1DB11E3D6A6BB85 CRC64;

Query Match 53.1%; Score 51; DB 3; Length 556;
 Best Local Similarity 62.5%; Pred. No. 4;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 TQETYGALDLCGASTQ 19
 Db 276 THSTVAVMDLGGASTQ 291

RESULT 10

09XI62 ID 09XI62 PRELIMINARY; PRT; 483 AA.

AC 09XI62; PRELIMINARY; PRT; 483 AA.

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE F7A19.34 protein.

GN F7A19.34

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.

NCBI_TaxID=3702;

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA;

RA Federici N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Altieri H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,

RA Gonzalez A., Kremenetskaia I., Kim C., Ienz C., Li J., Liu S.,

RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC007576; AND39311.1; -

DR InterPro: IPR000407; GDAI_CD39_NTPase.

DR InterPro: IPR001092; HIA_Basic.

DR Pfam: PF01150; GDAI_CD39; 1.

DR PROSITE: PS01238; GDAI_CD39_NTPASE; UNKNOWN.1.

DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN.1.

SO SEQUENCE 483 AA; 53425 MW; 4E31D13830F1C8F9 CRC64;

Query Match 51.0%; Score 49; DB 10; Length 483;
 Best Local Similarity 55.6%; Pred. No. 7.4;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 SDTQETYGALDLCGASTQ 19
 Db 212 TDPLETTGIVELGASAO 229

RESULT 11

09FU11 ID 09FU11 PRELIMINARY; PRT; 447 AA.

AC 09FU11; PRELIMINARY; PRT; 447 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Apyrase 2.

GN Apy2.

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

NCBI_TaxID=3888;

RN [1]

RP SEQUENCE FROM N.A.

RA Jin L., Roux S.J.;

RT Cloning of a Second Apyrase in Pisum sativum ";

DR Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF305783; AAG2204.1; -

DR InterPro: IPR000407; GDAI_CD39_NTPase.
 DR Pfam: PF01150; GDAI_CD39; 1.
 DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
 SO SEQUENCE 447 AA; 48783 MW; 5CB2B0CC7A7F860E CRC64;

Query Match 50.0%; Score 48; DB 10; Length 447;
 Best Local Similarity 52.9%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 DTQETYGALDLCGASTQ 19
 Db 187 DSDTVGVMDLGGASQ 203

RESULT 12

08R0U1 ID 08R0U1 PRELIMINARY; PRT; 448 AA.

AC 08R0U1; PRELIMINARY; PRT; 448 AA.

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Similar to lysosomal apyrase-like 1 (Fragment).

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RA Strausberg R.;

RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC026420; AAH26420.1; -

FT NON_TER

SO SEQUENCE 448 AA; 51285 MW; 0DA76F8BA734E3D6 CRC64;

Query Match 50.0%; Score 48; DB 11; Length 448;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 QETYGALDLCGASTQ 19
 Db 107 KRTAGVLDMGVSTQ 121

RESULT 13

09XFC9 ID 09XFC9 PRELIMINARY; PRT; 462 AA.

AC 09XFC9; PRELIMINARY; PRT; 462 AA.

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Mod factor binding lectin-nucleotide phosphohydrolase.

GN LMP.

OS Dolichos biflorus (Horse gram).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dolichos.

NCBI_TaxID=3840;

RN [1]

RP SEQUENCE FROM N.A.

RA TISSUE=ROOT;

RC MEDLINE=99254131; PubMed=10318974;

RA Ezler M.E., Kalsi G., Ewing N.N., Roberts N.J., Day R.B.;

RA Murphy J.B.;

RT "A mod factor binding lectin with apyrase activity from legume

roots".

RL Proc. Natl. Acad. Sci. U.S.A. 96:5856-5861(1999).

DR EMBL: AF139807; AAD31285.1; -

DR InterPro: IPR000407; GDAI_CD39_NTPase.

DR Pfam: PF01150; GDAI_CD39; 1.

DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.

DR Hydrolase; lectin.

SO SEQUENCE 462 AA; 51183 MW; 59F865A9D4CC444B CRC64;

